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Compugen
GenCore version (c) 1993 - 2004
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model 3 10 using search, protein OM protein •• 2004, 19:05:42 24, May on: Run

update Search time 51 Seconds (without alignments) 626.037 Million cell

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13

US-09-756-541-1 561 1 FYKVEAIVRPWRIO score: Title: Perfect so Sequence:

, VLPVSDVIRVRTGERGEKAB FYKVEAIVRPWRIQQVSSAL.

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residues 282547505 seds, 1586107 Searched:

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Database

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*

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### SUMMARIES

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	Ω	AAB69495	AAB69496	AAB69503	ABP79052	AAB69501	AAB69497	AAB69498	AAG93226	AAB69502	ADA34150	AAB69499	ABG24254	AAB69500	AAB79181		ABP03233	ABB49279	ABG24253	ABG24250	AAB69505		AAB69504	ABG24252	ABU49254	AAR05799
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RESULT 1

AAB69495 standard; protein; 113 AA

AAB69495; 

entry) (first 23-APR-2001

PII protein. thaliana Arabidopsis PII; plant nitrogen regulatory gene; P-PII; transgenic plant; herbicide screening. Arabidopsis thaliana; l nitrogen assimilation;

Arabidopsis thaliana

US6177275-B1.

23-JAN-2001,

97US-00899330. 23-JUL-1997; 96US-0022328P. 24-JUL-1996;

(UYNY ) UNIV NEW YORK STATE.

Hsieh M; Lam H, Coruzzi GM,

AAF58583. WPI; 2001-158572/16 N-PSDB; AAF58581, A Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 1; Fig 1; 35pp; English.

The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

Z 113 Sequence

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RESULT 4
                    RESULT 3
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Pred. No. 6.3e-56;
Score 551; DB 4; I
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              100.0%;
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en assimilation;
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Best Local
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been isolated.
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screening
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transgenic plant; herbicide s
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Pred. No. 3.7e-31;
}; Mismatches 24;
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                                                                                                                       strain PCC 7942 PII protein
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112
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standard, protein;
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for isolating
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[ (also called P-PII) nucleotide sequences have been isouseful for regulating nitrogen assimilation in plants,
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                                         Novel P-PII genes capable of regulating plant nitrogen useful for transgenic plant production, and as probes fadditional genomic clones having P-PII gene promoters.
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plant; herbicide sc
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Pred. No. 5.3e-28
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transgenic ;
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transgenic plan
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              2001-158572/16
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                                         P-PII
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                                                                                                    Example;
                                                                                                                                                                                                                                                                                                                       Query Match
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            WPJ ;
                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                 The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSBFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKVKI
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                                                                                                                                                                                                                                                ÖĘ
                                                                                                                                                                                                                                                 Le manufacture infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    brasiliense; PII; plant nitrogen regulatory gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                 from Neisseria gonorrheae, useful for theor treating or preventing N. gonorrheae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 308.5; DB 5,
Pred. No. 1.3e-30;
                                                                                                                                                                           Monaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azospirillum brasiliense PII protein.
                                                                                                                                                                                                                                                                                            528; 815pp; English.
                                                                                                                                                                         Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00899330
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                                                                                                                 2001GB-00003424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first en
  Neisseria gonorrhoeae
                                                                                                                                                                           Pizza M,
                                                                                                                                                                                                     2003-058415/05
)B; ABZ40022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lam H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                              CHIRON SPA
                                                                                                                                                                                                                                                                                           Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121 AA;
                            WO200279243-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Azospirillum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azospirillum
                                                                                                               12-FEB-2001;
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                                                                                    12-FEB-2002;
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medicament f
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23-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
                                                          10-CCT-2002
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Legood
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transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                                                                                                                                                                                KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVX
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I genes capable of regulating plant nitrogen assimilation, transgenic plant production, and as probes for isolating genomic clones having P-PII gene promoters.
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                                                                                                                                      112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nia coli; PII; plant nitrogen regulatory gene; P-PII assimilation; transgenic plant; herbicide screening
                                                                                                                                                                                                                                                              EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                     Indels
                                                                                                                                      DB 4;
                                                                                                                                                         7;
26;
                                                                                                                                    Score 284.5; DB - Pred. No. 1.3e-27, 7; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                      AAB69498 standard; protein; 112
                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 1; 35pp; English.
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                                                                                                                                      50.7%;
larity 50.9%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-158572/16
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli
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                                                                                                           A.A.
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                                                                                                           112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUL-1997;
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                                                                                                                                                                     56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitrogen
                                                                                                           Sequence
                                                                                                                                                                                                                                                               63
                                                                                                                                          Match
                                                                                                                                                        Local
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sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                        # 1
19
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              gene, measuring expression of a gene, analyzing or pattern of a gene and identifying homologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yokoi
                                                                                                                                                                                                                                          amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6980; 246pp + Sequence Listing; English.
                                                             EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ochiai
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46.8%; Pred. No. 7.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi
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                                                                                                                                                                                                                    SEQ
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2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                            2000EP-00127688
                                                                                                                                           standard; protein;
                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum.
                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mizoguchi H,
Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                             Coryneform bacterium; a
organic acid synthesis.
                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                    glutamicum
                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000;
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                                                                                                                                                                                            26-SEP-2001
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Tateishi
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50.7%; Score 284.5; 50.9%; Pred. No. 1.30 ive 27; Mismatches

27;

Conservative

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Similarity

Query Match Best Local S Matches 56

DB 4;

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                                                                                                                              Bush D;
                                                                                                                                                                                                                                                                                                       baumannii protein.
         biocontrol
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                          Acinetobacter
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                                                                                             09-JUN-1998;
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                                                            13-MAY-2003
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Best Local
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                                                                                                              gene; P-PI
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⊶
111
                                                                                                             Rhodobacter capsulatus; PII; plant nitrogen regulatory gene; nitrogen assimilation; transgenic plant; herbicide screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
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                                                                                                                                                                                                                                                                             Novel P-PII genes capable of regulating plant nitrogen assuseful for transgenic plant production, and as probes for additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 264.5; DB 4
Pred. No. 4.2e-25;
5; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acinetobacter baumannii protein #1311
                                                                                             protein.
                                          112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 124
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                                                                                                                                                                                                                                                                                                                 English
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                                          protein;
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                                                                                              PII
                                                                                                                                                                                                                                             Hsieh
                                                                            entry)
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                                                                                             capsulatus
                                                                                                                                       Rhodobacter capsulatus
                                                                                                                                                                                                                                                                                                                 1; 35pp;
                                                                                                                                                                                                                            NEW YORK
                                                                            (first
                                                                                                                                                                                                                                             Lam H,
                                                                                                                                                                                                                                                              2001-158572/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA34150 standard;
                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 112 AA;
                                                                                                                                                                                                                            CNIV
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                                         AAB69502
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                                                            AAB69502
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Best Local
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                          RESULT 9
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ADA3415
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSSEFSEDKFVAKVKME
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Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to isolated Acinetobacter baumannii nucleic
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32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328pp; English
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                                                                                       baumannii
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B; ADA30024.
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                                                                                                                                                                        The present sequence is encoded by a nitrogen regulatory PII gene. Nor plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clawith the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                                                                                                                                                                  KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                Novel P-PII genes capable of regulating plant nitrogen assimilat:
useful for transgenic plant production, and as probes for isolat:
additional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensic;
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genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                     109
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                                                                                                                                                                                                                                                                                                                                  111;
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                                                                                                                                                                                                                                                                                                                     Score 257; DB 4; Le
Pred. No. 3.7e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic protein #24245
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                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                     English
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23-AUG-2000; 2000US-00649167
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ilarity 47.7%;
Conservative 2'
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96US-0022328P
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                         (UYNY ) UNIV NEW YORK STATE
                                                  Hsieh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                     Example, Fig 1, 35pp;
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AAS88441.
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                                                                         WPI; 2001-158572/16
                                                  Lam H,
                                                                                                                                                                                                                                                                                                                                              Similarity
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  24-JUL-1996;
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                                                                                                                                                                                                                                                                                                            Sequence
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Best Local
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                                                  Cornzzi
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Matches
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed crivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal crivity of (III) or to treat disease states involving (II). (II) as polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRHGGSEFSEDKFVAKVKME
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إما
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 256.5; DB 4
Pred. No. 6.9e-24;
3; Mismatches 30
                            ID NO 54613; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum PII protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 160 AA;
                              SEQ
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biodiversity
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                            Claim
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme diagnosis; Corynebacterium diphtheriae; genetic engineering; Brevibacterium; environmental condition.
                                               solated.
                                  The present sequence is encoded by a nitrogen regulatory PII gene. Nor plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clawith the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                               KIEAIIKPFKLDEVRS-LSGVGLQGITVTEAKGFGRQKGHTDLYRGAEYIVD-FLPKVKI
                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                   Length 111
                                                                                                                                                                                                                                                                                   63 ELVVKKDOVESVINTILEGARIGEIGDGKIFVLPVSDVIRVRIGERG
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
                                                                                                                                                                                                          28
                                                                                                                                                                                 Score 256; DB 4;
Pred, No. 4.9e-24
26; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium glutamicum HA protein sequence
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99DE-01031636.
99DE-01032125.
99DE-01032126.
99DE-01032129.
99DE-01032129.
99DE-01032920.
99DE-01032928.
99DE-01032938.
99DE-01032933.
99DE-01032933.
99DE-01032933.
99DE-01032933.
           English
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                                                                                                                                                                                   45.68;
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           35pp;
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                                                                                                                                                                                               Similarity
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9-JUL-1999;
9-JUL-1999;
9-JUL-1999;
9-JUL-1999;
4-JUL-1999;
           ig
ig
                                                                                                                                                           Sequence 111
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             Example;
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis
and adaptation (HA) proteins given in AAB79023 to AAB79242. The C.
glutamicum HA genes (1) can be used in vectors for expression in host
cells and production of fine chemicals, such as, an organic acid,
proteinogenic or nomproteinogenic amino acid (preferred), purine or
pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
c pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
c pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
c pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
c pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated
c polyketide or enzyme. The amino acids produced can be lysine, glutamine,
c glutamate, alanine, leucine, isoleucine, serine, threonine, histidine,
c tyrosine, phenylalanine, or tryptophan. The fine chemical production can
be modulated. The presence or activity of Corynebacterium diphtheriae.
c for diagnosing the presence or activity of Corynebacterium diphtheriae.
c for genetically engineered Corynebacterium or Brevibacterium. The HA
c proteins encoded by the (1) are used to maintain homeostasis in C.
c proteins encoded by the microorganism to adapt to different environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                           can
used
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The HA
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vitamins
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line acids,
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H
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carbohydrates,
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                                                                                                                                                                                                  acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 246.5; DB 4;
Pred, No. 5.7e-23;
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                                                                                                                                                                                                 Corynebacterium glutamicum nucleic production of fine chemicals such nucleotides, lipids, fatty acids, c
                                                                                                                             Zelder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schroeder H,
                                                                                                                                                                                                                                                                       Claim 20; Page 563; 712pp; English.
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99DE-01033006.
99DE-01041378.
99DE-01041379.
99DE-01041390.
99DE-01041391.
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larity 50.6%;
Conservative
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(first ent
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                                                                                                                                                                                                              of
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14-JUL-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                                   New isolated modulation of
                                                                                                                                                                                                                             nucleosides,
                                                                                                   BASE
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16-MAY-2002
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                       in the identification or Lactococ
                                                                                                                     Ehrlich
                                                                                                                                                                                                                                           SEQ ID NO 1639; 2504pp; French
                                                                                   INST NAT RECH AGRONOMIQUE
                                                                                                                     Ъ,
                                                                                                                     Renault
                                                                                                                                                                                        New nucleotide sequence useful lactis and related species.
                 2000FR-00004630
                                                  2000FR-00004630
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                                                                                                                      Sorokine
                                                                                                                                                       WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112 AA;
                 11-APR-2000;
                                                  11-APR-2000;
                                                                                                                      Bolotine A,
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                                                                                  (INRG >
                                                                                                                                                                                                                                           Claim
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KVEAIVRPWRIQQVSSALLKIG-IRGVTVSDVRGFGAQGGSTERHGGSBFSEDKFVAKVK Gaps 2, Length 112; Indels 36; <u>ب</u> 40.1%; Score 225; DB 5 llarity 43.2%; Pred. No. 4e-20; Conservative 25; Mismatches 25; Similarity 48; Query Match Best Local S Matches 48 à

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61

В  $\delta$ 

g

Search completed: May 24, 2004, 19:13:02 Job time : 53 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                   Copyright
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using sw model protein search, 1 OM protein May 24, 2004, 19:10:08; Search time 14 Seconds (without alignments) 776.403 Million cell Run on:

updates/sec

US-09-756-541-1 561 1 FYKVEAIVRPWRIQQVSSAL. score: Sequence: Title: Perfect

....VLPVSDVIRVRTGERGEKAE

0.5 BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283366 seqs, 96191526 residues Searched:

hits satisfying chosen parameters oŧ Total number

seg length: 0 seg length: 200000000 DB DB Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\*
1: piri:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* 41 01 00 44 11 11 11 11 11

nted, No. is the number of results predicted by chance to have a greater than or equal to the score of the result being priderived by analysis of the total score distribution. . S score gand is Pred

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O.E.;

W.G.; Lenox, A.L.; Graham,

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GB: AE00065

PID:92982852;

30 259.5 46.3 112 2 AB0560 31 257.5 45.9 112 2 AG0381 32 257.5 45.9 112 2 AG0381 34 256.5 45.7 112 2 B64775 35 256.5 45.7 112 2 B64775 36 256.5 45.7 112 2 B64775 37 256.5 45.7 112 2 B69188 40 255.5 44.7 116 2 A33600 41 250.5 44.7 116 2 AD2915 42 245.5 43.8 B5 2 S76404 43 238.5 42.5 114 2 B87313 44 238.5 42.5 114 2 B87313 45 225 40.1 113 2 G86823	nitrogen regulator	nitrogen regulator								nitrogen regulator	nitrogen regulator	tei	nitrogen regulator	re		nitrogen regulator
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259.5 46.3 1 257.5 45.9 1 257.5 45.9 1 256.5 45.7 1 256.5 45.7 1 256.5 45.7 1 256.5 45.7 1 250.5 44.8 1 245.5 44.7 1 225.40.1 1	N	C1	N	N	N	N	N	N	C)	N	7	N	~	N	N	7
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## AL I GNMENTS

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RESULT 1
D85024
P II nitrogen sensing protein GLB I [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: D85024
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85024
A;Accession: D85024
A;Molecule type: DNA
A;Residues: 1-196 <STO>
A;Cross-references: GB:NC_001268; NID:g7268574; PIDN:CAB80683.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4901900
A;Map position: 4
                                                                                                                                               Cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
P70310
nitrogen regulatory protein P-II - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 26-Aug-1999
C;Accession: F70310
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus
A;Reference number: A70310; MUID:9819666; PMID:9537320
A;Accession: F70310
A;Accession: F70310
A;Accession: F70310
A;Accession: F70310
A;Accession: F70310
A;Accession: F70310
A;Cross-references: GB:AE000674; NID:g2982850; PIDN:AAC06473.1; PID:g2982852; GF
A;Experimental source: strain VF5
C;Genetics:
A;Gene: glnB
C;Superfamily: regulatory protein P-II
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Pred. No. 6.8e-48
Mismatches 0
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GB:AE002098; NID:g7227249; PIDN:AAF42322.1; PID:g72272:
B, strain MC58
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-112 < TSI>
A; Cross-references: GB: M62447; NID: g154517; PIDN: AAA27312.1; PID: g552028
A; Cross-reference: PCC 7942
A; Note: the authors translated the codon CCT for residue 83 as Thr
B; Li, N.; Warren, P.V.; Golbeck, J.H.; Frank, G.; Zuber, H.; Bryant, D.A.
Biochim. Biophys: Acta 1059, 215-225, 1991
A; Title: Polypeptide composition of the Photosystem I
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                                                                                                                                                                                                                                                                                                                                                                                  Litrogen regulatory protein P-II NMB1995 [similarity] - Neisseria meningitic C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Accession: B81019
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E. Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Doug ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizz Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rapg A; Title: Complete genome sequence of Neisseria meningitidis serogroup B stra A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Accession: B81019
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-112 <TET>
A; Cross-references: GB:AE002548; GB:AE002098; NID:g7227249; PIDN:AAF42322.1; A; Experimental source: serogroup B, strain MC58
C; Genetics:
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                                                                                                                                                   3 KIEAIVKPFKLDDVREALTEIGITGMTVSEVKGFGRQKGHTEIYRGAEYAVD-FLPKVKI
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C; Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_chan C; Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_chan C; Accession: A39696; F56817
R; Tsinoremas, N.F.; Castets, A.M.; Harrison, M.A.; Allen, J.F Proc. Natl. Acad. Sci. U.S.A. 88, 4565-4569, 1991
A; Title: Photosynthetic electron transport controls nitrogen A; Reference number: A39696; MUID:91271233; PMID:1905010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Tyr) (covalent) #status predicted
                       Score 308.5; DB 2;
Pred. No. 2.6e-23;
i Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 54.8%; Score 307.5; DB 2; Similarity 54.5%; Pred. No. 3.2e-23; 60; Conservative 25; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: NMB1995
C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein
F;51/Binding site: UMP (Tyr) (covalent
                                                                       24;
                         55.0%;
larity 55.5%;
Conservative
                                                  Similarity
                                                                         61;
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Best Local S
Matches 60
                         Query Match
Best Local S
Matches 61
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A;Residues: 1-112 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74018.1; PID:g17131411; GSPDB:GN0017
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L, M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83744.1; serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                               nitrogen regulatory protein P-II glnB [imported] - Nostoc sp. (strain PCC 7: Species: Nostoc sp. PCC 7120
C; Species: Nostoc sp. PCC 7120
A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7: Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C; Accession: AH2095
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, Norazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, Nakazaki, N.; Shimpo, S.; MulD:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nitrogen regulatory protein P-II NMA0447 [similarity] - Neisseria meningiti
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81961
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee
                                                                                                                                                                          VAKVKM
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                                                                                                                                                                                                   111
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A; Title: Complete DNA sequence of a serogroup A strain of Neisseria A; Reference number: A81775; MUID: 20222556; PMID: 10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 112;
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C;Genetics:
A;Gene: glnB; NMA0447
C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein
F;51/Binding site: UMP (Tyr) (covalent) #status predicted
ignal transduction (covalent) #status predicted
                                                                      DB 2;
                                                                       58.4%; Score 327.5; DB 2;
larity 54.5%; Pred. No. 3.5e-25;
Conservative 30; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.8%; Score 318.5; DB 2;
larity 57.3%; Pred. No. 2.7e-24;
Conservative 24; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory protein P-II
                                                                                                                       30;
  C; Keywords: phosphoprotein; signal F;51/Binding site: UMP (Tyr) (coval
                                                                                                  Similarity
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A, Status: preliminary
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C,Superfamily:
                                                                         Query Match
Best Local S
Matches 60
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Best Local S
Matches 63
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          Zamaroczy, M.; Delorme, F.; Elmerich, C.
Gen. Genet. 224, 421-430, 1990
:le: Characterization of three different nitrogen-regulated promoter
:erence number: S13078; MUID:91094780; PMID:1702507
                                                                                                                                                                                                                                          PID:938665
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                                                                                                                                                                                                                                                                                                                                                                                 increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th Similarity 49.1%; Score 287.5; DB Similarity 49.1%; Pred. No. 3e-21; 54; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                transduction
                                                                                                                                                                                                                                 Cross-references: EMBL:X51499; NID:g38664; Experimental source: strain SP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (covalent)
                                                                                                                                                                                                                                                                                                                                                                          Description: P-II protein synthesis : Superfamily: regulatory protein P-II Keywords: phosphoprotein; signal tran 51/Binding site: UMP (Tyr) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
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       R;de Zamaroczy, M.; D
Mol. Gen. Genet. 224,
A;Title: Characteriza
A;Reference number: S
A;Accession: S13078
A;Accession: S13078
A;Accession: S13078
A;Accession: S13078
A;Accession: S13078
A;Coss-references: B
A;Experimental source
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Function:
A;Description: P-II p
C;Superfamily: regula
C;Keywords: phosphopr
F;51/Binding site: UM
                                                                                                                                                     preliminary
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Best Local S
Matches 54
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C, Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 24-Aug-2001
C; Accession: D82102
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dods Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; S. Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio choler A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Reference number: A82035; MUID:20406833; PMID:10952301
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-114 - HEI>
A; Cross-references: GB:AE004295; GB:AE003852; NID:g9656789; PIDN:AAF95383.1; GS
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
A; Genetics:
A; Genetic
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S13078
nitrogen regulatory protein P-II - Azospirillum brasilense
C; Species: Azospirillum brasilense
C; Species: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-Aug
                                                                                                                                                                                                                                                                                          the spec
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ArReference number: A56817; MUID:91355213; PMID:1653017
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64 EIVVTDDVADRCVDTIIETAQTGKIGDGKIFITNVERVVRIRTGEEDEDA
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Pred. No. 1.9e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.6%; Score 306.5; DB 55.5%; Pred. No. 4e-23; ive 23; Mismatches
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57; Conser
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(strain 0157:H7, substrain
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                                                                                        KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
                                                                                                                   C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001 C; Accession: AF0354
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; F deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                   Gaps
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-112 < XUR>
A; Cross-references: GB: AL590842; PIDN: CAC92161.1; PID: g15980875; C; Genetics:
A; Gene: glnB
C; Superfamily: regulatory protein P-II
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26:
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Pred. No. 5.9e-21;
7; Mismatches 26;
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Pred. No. 5.9e-21;
3; Mismatches 26;
       5.9e-21
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C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001
      Pred. No. 5.96
'; Mismatches
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illarity 50.9%;
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larity 50.0%;
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      50.9%;
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    Similarity
56; Conser
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A;Gene: ECs3419
C;Superfamily:
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C;Genetics:
A;Gene: glnB
C;Function: <GEN>
A;Gene: this protein pathway
A;Note: this protein participates indirectly in activation of glutamine synthase activit A;Note: under nitrogen-limiting conditions it is covalently uridylylated; in nitrogen extransferase / uridylyl-removing enzyme which is regulated by the glutamine/alpha-ketoglu
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C;Function:
A;Description: important for the control of glutamine synthase; in nitrogen-limiting con
to form P-II-UMP; P-II-UMP allows the deadenylation of glutamine synthetase, thus activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activates transcription of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Function: <NTRB>
A;Description: <NTRB>
A;Description: de-uridylylated P-II forms a complex with nitrogen regulation the uridylylated form of P-II forms a complex with ntrB; free ntrB phosphory A;Note: phosphorylated nitrogen regulation protein I (ntrC) activates transcrC;Function: <ATR>
A;Description: uridylylated P-II forms a complex with adenylyltransferase; thy ylyltransferase deadenylylates glutamine synthase
A;Note: free glutamine synthase is active; adenylylated glutamine synthase is C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein; signal transduction
F;Si/Binding site: UMP (Tyr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig-1999
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C;Species: Klebsiella pneumoniae
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-C;Accession: 504377
K;Holtel, A.; Merrick, M.
Mol. Gen. Genet. 215, 134-138, 1988
A;Title: Identification of the Klebsiella pneumoniae glnB gene: ruc
A;Reference number: S04376; MUID:89201233; PMID:2907369
A;Accession: S04377
A;Molecule type: DNA
A;Residues: 1-112 <HOL>
A;Cross-references: EMBL:X14512; NID:943804; PIDN:CAA32177.1; PID:9
A;Genetics:
A;Genetics:
A;Genetics:
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                                                      C.A.; Petna, N.T.;
   NID:g49395; PIDN:CAA79890.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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;Species: Klebsiella pneumoniae
;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_
                    A; Experimental source: strain K-12, substrain W3110 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pefna, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia co. A; Reference number: A64720; MUID:97426617; PMID:9278503 A; Accession: H65032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.7%; Score 284.5; DB 1; 50.9%; Pred. No. 5.9e-21; ive 27; Mismatches 26;
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C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein; signal transduction
F;51/Binding site: UMP (Tyr) (covalent) #status
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EMBL: 221843;
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-references:
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Query Match

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S04377 nitrogen

A; Note:

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Prentice, M.B .; Dougan, G.; , S.; Barrell,

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completed: May 24, 2004, 19:15:40
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                                                                                                                                nitrogen regulatory protein p-II STY2808 [imported] - Salmonella enterica subsp. enteric
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2061 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AHC826
B;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connertor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
th, T.; Connertor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Skelton, J.; Stevens, K.;
Alaute, Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Accession: AHO826
A;Accession: AHO826
A;Accession: AHO826
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-112 <PAR>
A;Gross-references: GB:AL513382; PIDN:CAD02764.1; PID:g16503774; GSPDB:GN00176
C;Genetics:
A;Gene: STY2808
C;Superfamily: regulatory protein P-II
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3 KIDAIIKPFKLDDVREALAEVGITGMTVTEVKGFGRQKGHTELYRGAEYMVD-FLPKVKI
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larity 50.9%; Pred. No. 5.9e-21;
Conservative 27; Mismatches 26;
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RESULT 15
G85900
kypothetical protein glnB [imported] - Escherichia coli (strain O157:H7, substrain ED193)
C,Species: Escherichia coli
C,Species: Escherichia coli
C,Bate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C,Accession: G85900
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhemiler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Bscherichia coli O157:H7.
A;Reference number: A85480; MUD:21074935; PMID:11206551
A;Accession: G85900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 STDA
A;Residues: 1-12 STDA
A;Residues: 1-12 STDA
A;Residues: 1-12 STDA
A;Reperimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: GlnB
C;Superfamily: regulatory protein P-II
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 KVEAIIRPEKLEIVKKALSDAGYVGMTVSEVKGRGVQGGIVERYRGREYIVD-LIPKVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
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Pred. No. 1.2e-20;
5; Mismatches 27
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Compugen Ltd
GenCore version (c) 1993 - 2004
          Copyright
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- protein search, using sw model OM protein

; Search time 10.5 Seconds
 (without alignments)
560.374 Willion cell updat May 24, 2004, 19:06:17 Run on:

es/sec

113

.....VLPVSDVIRVRTGERGEKAE

US-09-756-541-1 561 1 FYKVEAIVRPWRIQ Title: Perfect

score:

FYKVEAI VRPWRIQQVSSAL..

Sequence:

Gapext BLOSUM62 Gapop 10.0 , Scoring table:

52070155 residues 0.5 141681 segs, Searched:

141681 hits satisfying chosen parameters: ų. O Total number

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES		
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Tandeau de Marsac N.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF HEN P-II
IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY).

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN
TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS
THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING
THE ENZYME (BY SIMILARITY).
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PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND LIGHT QUALITY (BY SIMILARITY).
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Pfam; PF00543; f.

PRINTS; PR00340; PIIGLNE.

PRODOM; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

PROSITE; PS006496; PII GLNB CTER; 1.

PROSITE; PS006496; PII GLNB UMP; 1.
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                              Indels
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                                            DB 1;
                                       58.4%; Score 327.5; DB 1;
54.5%; Pred. No. 2.5e-26;
iive 30; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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No. 2.6e-25;
0E44B4B171A6233B
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Nitrogen regulatory protein P-II (PII signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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INTERPRO; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
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HSSP; P05826; 2PII.
                                                                                            Conservative
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60; Conserv
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE 29133 / PCC 73102;

MEDLINE=98304077; PubMed=9639924;

Hanson T.E., Forchhammer K., Tandeau de Marsac N., Meeks J.C.;

Hanson T.E., Forchhammer K., Tandeau de Marsac N., Meeks J.C.;

The strain ATCC 29133; glnB or the PII protein may be essential.";

Microbiology 144:1537-1547(1998).

Strain ATCC 29133; glnB or the PII protein may be essential.";

Microbiology 144:1537-1547(1998).

Strain ATCC 29133; glnB or the PII protein may be essential.";

Microbiology 144:1537-1547(1998).

STRAINA THE GS

C-1- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE PROSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY).

SPHOSPHORYLATED THESE EVENTS ARE REVERSED (BY SIMILARITY).

TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING THE ENZYME (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homotrimer (By similarity).
PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL LIGHT QUALITY (BY SIMILARITY).
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PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

Transcription regulation; Nitrogen fixation; Phosphorylation

MOD_RES 49 49 PHOSPHORYLATION (PROBABLE).
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                          FIVVEDNOVDMVVDKIIAAARTGEIGDGKIFISPVEQVVRIRTGEKNTEA
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larity 57.3%; Pred. No. 3.2e-25;
Conservative 23; Mismatches 23
                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Nitrogen regulatory protein P-II (PII signal
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                                                                                                                                                                                                                                                                                                                                                                                                     Tsinoremas N.F., Castets A.M., Harrison M.A., Allen J.F.,
Tandeau de Marsac N.;
"Photosynthetic electron transport controls nitrogen assimilation
cyanobacteria by means of posttranslational modification of the gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vitro kinase activity.";
J. Bacteriol. 177:5812-5817(1995).

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE G. GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN PIS PHOSPHORYLATED, THESE EVENTS ARE REVERSED.

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALL THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATINE ENZYME.
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STRAIN=PCC 7342;
MEDLINE=94110245; PubMed=8282715;
Forchhammer K., Tandeau de Marsac N.;
"The PII protein in the cyanobacterium Synechococcus sp. strain P 7942 is modified by serine phosphorylation and signals the cellul N-status.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-30.
STRAIN=PCC 6301;
MEDLINE=90249505; PubMed=2110911;
Harrison M.A., Keen J.N., Findlay J.B.C., Allen J.F.;
"Modification of a glnB-like gene product by photosynthetic elect transport in the cyanobacterium Synechococcus 6301.";
FEBS Lett. 264:25-28(1990).
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                                                                                                                                                                                                       (Anacystis nidulans R2),
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                                                                                                                                                                                                                              nidulans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inoue K., Bryant D.A.; "Genes biogenesis."; "Genes required for c-type cytochrome biogenesis."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                         Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91355213; PubMed=1653017;
Li N., Warren P.V., Golbeck J.H., Frank G., Zuber H., "Polypeptide composition of the Photosystem I complex Photosystem I core protein from Synechococcus sp. PCC Biochim. Biophys. Acta 1059:215-225(1991).
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sp. (strain PCC 6301)
                           PRT;
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STRAIN=PCC 7942;
MEDLINE=91271233; PubMed=1905010;
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28-FEB-2003 (Rel. 41, Last annota
Nitrogen regulatory protein P-II
                                                                               Created)
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J. Bacteriol. 176:84-91(1994)
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TaxID=1140, 1139;
                            STANDARD;
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Bacteria; Cyar
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STRAIN=PCC
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MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Yamada M., Yasuda M.,
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CRC64;
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                           family
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5F44B64CBFF3C559
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PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

Transcription regulation; Nitrogen fixation; I amon RES 49 49 PHOSPHORYLATION.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitrogen regulatory protein P-II (PII signal
                           protein
                             P(II)
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PhosSite; P80016; -.
InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_Pfam; PF00543; P-II; 1.
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MEDLINE=98088000; PubMed=9426594;
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EMBL; AF079137; AAF04333.1;
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LIGHT QUALITY.
SIMILARITY: Belongs
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FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-INFHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY) FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH A THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVI
                                                                                                                           SUBUNIT: Homotrimer (By similarity).
PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SP
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MEDLINE=21145866; PubMed=11248100;
MAAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur "Complete genomic sequence of Pasteurella mulcocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-11 CATALY CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THE ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THE ACTIVATOR OF GLNA.
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InterPro; IPR002332; PII glnB.UMP.S.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation; Phosphorylation;
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NO. 8.2e-25;
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Pasteurellaceae; Pasteurella.
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R Prints; PR00340; PIIGLNB.
R ProDom; PD001194; PII_GlnB_UMP; 1.
R PROSITE; PS00496; PII_GLNB_UMP; 1.
RPCSITE; PS00638; PII_GLNB_CTER; 1.
RPCSITE; PS00638; PII_GLNB_CTER; 1.
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RPCSITE; PS006496; PII_GLNB_
  VHICH CAUSES THE NE, SO ACTIVATING
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
NCBI_TaxID=192;
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"Characterization of three different nitrogen-regulated promoter
regions for the expression of glnB and glnA in Azospirillum
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                 DECREASES, P-II IS URIDYLYLATED TO P-II-JMP, WHIC
DEADENYLYLATION OF GLUTAMINE SYNTHETASE BY GLNE,
ENZYME (BY SIMILARITY).
                                                                            ENZYME (BY SIMILARITY).
SUBUNIT: Homotrimer (By similarity).
PTM: Uridylylated/deuridylylated by glnD (By similarity: Belongs to the P(II) protein family
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Bozouklian H., Elmerich C.;
"Nucleotide sequence of the Azospirillum brasilense
synthetase structural gene.";
Biochimie 68:1181-1187(1986).
-:- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN
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29.;
     THE RATIO OF GLW
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Pred. No. 1.4e-
1; Mismatches
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     EVENTS ARE REVERSED.
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Rest Local Similarity
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01-MAY-1991
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commercial
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    TO P-II-UMP
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PII protein and nucleotide sequenc
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        P-II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.

FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED.

SUBUNIT: Homotrimer (By similarity).

SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                   for
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                                                                                                                                                                          EMBL
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                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
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 P-II IS URIDYLYLATED
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Pred. No. 2.8e-22;
7; Mismatches 28
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InterPro; IPR002187; PII glnB.

InterPro; IPR002332; PII glnB.UMP_S.

Pfam; PF00543; P-II; 1.

PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

Transcription regulation; Witrogen fixation.
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Escherichia coli C6,
Escherichia coli C157:H7,
Salmonella typhimurium,
Salmonella typhi, and
Shigella flexneri.
Bacteria: Proteobacteria, Gammaproteobacteria:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nitrogen regulatory protein P-II 1.
GLNB OR B2553 OR C3076 OR Z3829 OR ECS3419 OR
T0295 OR SF2600 OR S2772.
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21, Last sequence up
42, Last annotation
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Purification and properties of PII pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602,
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DECREASES,
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MEDLINE=87250488; PubMed=2885322;
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NCBI_TaxID=562, 217992, 83334,
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49.1%;
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TO 2-KETOGLUTARATE
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S13078.
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54; Conser
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01-MAR-1992 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                       EMBL; X51499;
EMBL; M26107;
PIR; S13078; S
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SPECIES=E.coli; STRAIN=K12;
MEDLINE=91238719; PubMed=2034230;
Vasudevan S.G., Armarego W.L.F., Shaw D.C., Lilley P.E., Dixon N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednence
                                                                                                 Holtel A., Merrick M.;
"Identification of the Klebsiella pneumoniae glnB gene: nuclectide
sequence of wild-type and mutant alleles.";
Mol. Gen. Genet. 215:134-138(1988).
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Mitsuhashi N
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MEDLINE=97349980; PubMed=9205837;
Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N. Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada Yamagata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia "Construction of a contiguous 20.0-68.8 min on the linkage map an analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;

SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller J.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=E.coli; STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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N. H. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12. Science 277:1453-1474(1997).
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K-12."
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haemoglobin-like protein in Escherichia coli
Mol. Gen. Genet. 226:49-58(1991).
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on of the Escherichia
175:7441-7449(1993).
  gene.";
262:8690-8695(1987)
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                                                                                    PubMed=2907369
                                                                                                                                                                                                                                                          Poole R.K.; "Isolation and nucleotide
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                                                   C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                            SPECIES=E.coli;
MEDLINE=94042920; P
Liu J., Magasanik B
"The glnB region of
J. Bacteriol. 175:7
                                                                                                                                                                                                                                                                                                                                                FROM N.A.
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                                                                   SPECIES=E.coli;
MEDLINE=89201233;
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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                          SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Tida T., Takami H., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S. Lyphimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreill Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Laym Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S. typhi; STRAIN=CT18; MEDLINB=21534947; PubMed=11677608; MEDLINB=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wachill J., Dougan G., James K.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strain and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of a multiple drug resistant Salmonell enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
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G. III, Rose D.J., Darling A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-12 FROM N.A.
SPECIES=E.coli; STRAIN=K12 / W3110;
MEDLINE=94018640; PubMed=8412694;
van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.;
"The genes of the glutamine synthetase adenylylation cascade regulated by nitrogen in Escherichia coli.";
Mol. Microbiol. 9:443-458(1993).
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SPECIES=S.flexneri; STRAIN=2457T / ATCC
MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goldberg M.B., Burland V., G., Mayhew G.F., Plunkett
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Fournier
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RAKER BERKER BER
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KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
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Holtentification of the Klebsiella pneumoniae glnB gene: nuclectide sequence of wild-type and mutant alleles.";
Mol. Gen. Genet. 215:134-138(1988).

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLNN TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP.

P-II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-II IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transducing protein PII.";
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                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                                                                                            Vasudevan S.G., Gedye C., Dixon N.E., Cheah E., Carr P.D.,
Suffolk P.M., Jeffrey P.D., Ollis D.L.;
"Escherichia coli PII protein: purification, crystallization and
                                     Shigella
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#1
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No. 5.6e-22;
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Enterobacteríaceae, Klebsiella.
NCBI_TaxID=571;
   S.M., Runyen-Janecky.R.;
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on update)
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Mau B., Perna N.T., Payne S.M., Runyen-Jan
Schwartz D.C., Blattner F.R.;
"Complete genome sequence and comparative
flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
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(Rel. 12, Last sequence up
(Rel. 42, Last annotation
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                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOSLOS
SPECIES=E.coli;
MEDLINE=95171116; PubMed=7866749;
Thank E., Carr P.D., Suffolk P.M.,
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Pred.
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                                                                                                                                  SPECIES=E.col1;
MEDLINE=90089474; PubMed=2574599;
                                                                                                                                                                                                                                                        CRYSTALLIZATION, AND SUBUNITS.
SPECIES=E.coli;
MEDLINE=94123764; PubMed=8293810;
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                                                                                                                                                     50.7%;
                                                                                                                                                                                                                                                                                                                                                                   oligomeric structure.";
FRBS Lett. 337:255-258(1994)
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                                                                                                           REVIEW.
SPECIES=E.coli
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01-0CT-1989
01-0CT-1989
10-0CT-2003
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S73175.
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HSSP; P38504; 1GNK.
TIGR; MJ0059; -.
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HSSP; P05826;
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Eukaryota; 1
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Best Local S
Matches 59
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                                                                                                                                                                 commercial
                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
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  THESE EVENTS ARE REVERSED
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical nitrogen regulatory PII-like protein MJ0059.
MJ0059.
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Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC15D58A2P225507 CRC64;
          SUBUNIT: Homotrimer (By similarity).
SIMILARITY: Belongs to the P(II) protein family.
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SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 284.5; Db 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          fixation.
                                                                                                                                        use by non-profit institutions as los modified and this statement is not remontities requires a license agreement (or send an email to license@isb-sib.ch)
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ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen
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PII_GlnB_UMP
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    TO P-II-UMP,
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PIR; S04377; S04377.
HSSP; P05826; 2PII.
InterPro; IPR002187; P
InterPro; IPR00232; P
  URIDYLYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 AA;
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                                                                                                                                                                                                                                         X14012;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome.";
Plant Mol. Biol. Rep. 13:333-335(1995).
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELYVYKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
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Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) .
CRC64 ;
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SUBUNIT: Homotrimer (By similarity).
SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 53.6%; Pred. No. 8.9e-22; 9; Conservative 21; Mismatches 29;
                                                                                                                                                                                                                                                                                 InterPro; IPR002187; PII glnB.
Pfam; PF50543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB_CTER; 1.
Hypothetical protein; Transcription regulation; BINDING 51 51 UMP (BY SIMILARITY) SEQUENCE 112 AA; 12490 MW; 3DC3F307C32FE9F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Nitrogen regulatory protein P-II.
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                                                                                                                                                             U67464; AAB98041.1;
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                                                                                                                                                                                                             Gaps
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STRAIN=ATCC 11170 / S1;

Zhang Y., Ludden P.W., Roberts G.P.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYN-I-SUBUNIT: Homotrimer (By similarity).

-!- SUBUNIT: Homotrimer (By similarity).
                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales
Rhodospirillaceae; Rhodospirillum.
NCBI_TaxID=1085;
                                                                                                                                                                                                                                                                                                       112
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                                                                                                                                                                             Length
                                                                          PROSITE; PS00496; PII_GLNB_UMP; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
Transcription regulation; Nitrogen fixation; Chloroplast
BINDING 51 51 UMP (BY SIMILARITY).
BINDING 112 AA: 12320 MW; 29416AA49FC37A18 CRC64;
                                                                                                                                                                                                            Indels
                                                                                                                                                                 49.8%; Score 279.5; DB 1; 51.8%; Pred. No. 1.8e-21; winnstebes 31;
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35, Last sequence update \
37, Last annotation update \
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STRAIN=ATCC 11170 / S1;
MEDLINE=96254013; PubMed=8704966;
Johansson M., Nordlund S.;
"Transcription of the glnB and glnA gebacterium Rhodospirillum rubrum.";
Microbiology 142:1265-1272(1996).
                  ഗ
                  UMP
                                                              1, 1.
1 UMP; 1
3 CTER;
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InterPro; IPR002382; PII glnB.
InterPro; IPR002332; PII GlnB Un
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP;
PROSITE; PS00638; PII GLNB UMP;
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; S52328; S52328.
9; P05826; 2PII.
erPro; IPR002187; PII_9
                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                         Similarity
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01-NOV-1997
15-DEC-1998
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HSSP; P058:
InterPro;
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Best Local
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Zinchenko V.V., Churin Y., Shestopalov V.I., Shestakov S.V.;
"Nucleotide sequence and characterization of the Rhodobacter
sphaeroides glnB and glnA genes.";
Microbiology 140:2143-2151{1994}.

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE
GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS MR-II CATALYZED
CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL
ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE
DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE
DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME.
-!- SUBUNIT: Homotrimer (By similarity).
-!- SUBUNIT: Belongs to the P(II) protein family.
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                                                                                                                                                                                                                                                            transducing protein)
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                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodoba
Rhodobacteraceae; Rhodobacter.
                                                                                                                                    CRC64
                                                                                                                                                                       49.3%; Score 276.5; DB 1;
larity 48.2%; Pred. No. 3.6e-21;
Conservative 27; Mismatches 29;
                                                                                                                       (BY SIMILARITY)
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InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII glnB.
Ffam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tion update)
InterPro; IPR002332; PII_GlnB_UMP_S.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII_glnB; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
Transcription regulation; Nitrogen fixation.
BINDING 51 51 UMP (BY SIMILA)
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01-NOV-1995 (Rel. 32, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
Nitrogen regulatory protein P-II (PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7921264
                                                                                                                            51
12420 MW;
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                                                                                                                                          A.A.
                                                                                                                                                                                        Similarity
53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE=95005468;
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S33180; S
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Best Local
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P05826; 2PII
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STRAIN=RCR2011 / S
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EMBL; AL591787;
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NCBI TaxID=382;
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collbetween the Swiss Institute of Bioinformatics and the EMBL out the European Bioinformatics Institute. There are no restriction use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contities requires a license agreement (See http://www.isb-sib.ch/or send an email to license@isb-sib.ch).
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Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                      CRC64;
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Science 273:1058-1073(1996).
-1- SIMILARITY: Belongs to the P(II) protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation update) regulatory PII-like protein
                                                                          DB 1;
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Pfam; PF00543; P-II; 1.

PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

Hypothetical protein; Transcription regulation;

Hypothetical protein; Transcription regulation;

BINDING 51 51 51 UMP (BY SIMILARITY)

BINDING 51 51 51 SIMILARITY)
IP (BY SIMILARITY)
B278486AC9EB17D3
                                                                       Score 276.5; DB 1
Pred. No. 3.6e-21;
8; Mismatches 30
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HSSP; P38504; 1GNK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=2139650'; FUDREGE=11461430;

Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

A Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kabn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,

Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;

Tanalysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021.";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

C -: FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN

C -: FUNCTION: IN NITROGEN-LIMITING CONDITIONS, THE RATIO OF GS.,

THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-II

IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.

C -: FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS

GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO

NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II

IS URIDYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED.

C -: SUBUNIT: Homotrimer (By similarity).

C -:- SUBUNIT: Belongs to the P(II) protein family.
61
3 KVEAIIRPEKLEIVKKALSDAGYVGMTVSEVKGRGVQGGIVERYRGREYIVD-LIPKVKI
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IP (BY SIMILARITY).
85E6465E64B57001 CRC64;
                                                                     108
                                                                                                                                                                                                                                                                                             Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                STRAIN=RCR2011 / SU47;
MEDLINE=97085050; PubMed=8931324;
Arcondeguy T., Huez I., Fourment J., Kahn D.;
"Symbiotic nitrogen fixation does not require acglutamine synthetase I in Rhizobium meliloti.";
FEMS Microbiol. Lett. 145:33-40(1996).
                                                                                                                                                                                                                                            update)
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01-NOV-1997 (Rel. 35, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Nitrogen regulatory protein P-II.
GINB OR R01639 OR SMC00947.
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STRAIN=1021;
MEDLINE=21396507; PubMed=11481430;
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InterPro; IPR002332; PII_GlnB_U
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII_glnB; 1.
PROSITE; PS00496; PII_GLNB_UMP;
PROSITE; PS00638; PII_GLNB_UMP;
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Matches 52; Conservative 27; Mismatches 27; Indels 1; Gaps 1;

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RYEAIVRPWRIQQVSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM 52

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### ALIGNMEN'

Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M. Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. 01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PII protein (P II nitrogen sensing protein GLB I) (At4g01900%.
T7B11.16 OR AT4G01900.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. M.D., Huang E.N., Nascimento L., de la Bastide M., Habermann K., Vil M Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A., O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Schutz K., Parnell L.D., Dedhia N.N., McCombie W.R.; "Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A.
MEDLINE=99030678; PubMed=9811909;
Hsieh M.H., Lam H.M., van de Loo F.J., Coruzzi G.;
Hsieh M.H., Lam H.M., van de Loo F.J., Coruzzi G.;
"A PII-like protein in Arabidopsis: putative role in nitrogen sensing.";
Proc. Natl. Acad. Sci. U.S.A. 95:13965-13970(1998). 196 AA PRT; PRELIMINARY; SEQUENCE FROM N.A. STRAIN=cv. Columbia; SEQUENCE FROM N.A. SEQUENCE FROM N.A sids II; Bra TaxID=3702; O9ZST4; 01-MAY-1999 ( 01-MAY-1999 ( 01-JUN-2003 ( PII protein ( T7B11.16 OR A eurosids NCBI TaxI Q9ZST4 TSZ60 

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NCBI_TaxID=74547;
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01-JUN-2001
01-JUN-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                PII protein
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Best Local S
Matches 96
               Query Match
Best Local S
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PII protein (Fragment).
Ricinus communis (Castor bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Euchophyta; Core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalypheae;
Ricinus.
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                                                                                                                         S. A. S.
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                                                              Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c)
                                                                                                                                                                          Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORF clones.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF095455; AAC7833.1; -.
EMBL; AC007138; AAD22652.1; -.
EMBL; BT005209; AAO63273.1; -.
EMBL; BT005209; AAO63273.1; -.
EMBL; BT005209; AAO63273.1; -.
EMBL; BT005209; Aco63273.1; -.
EMBL; BT005209; Acc63014.
EMBL; BT005209;
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                   databases
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EMBL; AP095454; AAC78332.1; -.

HSSP; P05826; 2PII.

GO; GO:0030234; F:enzyme regulator activity; IEA.

GO; GO:0006808; P:regulation of nitrogen utilization;
InterPro; IPR002187; PII_glnB.

Pfam; PF00543; P-II; 1.
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MEDLINE=99030678; PubMed=9811909;
Hsieh M.H., Lam H.M., van de Loo F.J., Coruzzi G.;
"A PII-like protein in Arabidopsis: putative role in sensing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 561; DB 10;
Pred. No. 4.5e-48;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PROG340; PIGENB.
PRODOM; PDC01194; PII glnB; 1.
PROSITE; PSC0638; PII GLNB CTER; 1.
SEQUENCE 196 AA; 21275 MW; PE740EA66776F157
Arabidopsis sequencing project;
pritted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence up (TrEMBLrel. 24, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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|| Similarity 100.0%;
|113; Conservative (
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PROSITE; PS00638; PII
NOW_TER
                                                                                                                                                                                                                                                                                                                                                                                                  PF00543; P-II;
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                                                     SEQUENCE FROM N.A.
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01-MAY-1999
01-JUN-2003
                  Submitted
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Best Local
Matches 11
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                                                                                                          FYKVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKV
                                                                                   PYKVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKV
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

NCBI_TaxID=3879;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae
   Length 197;
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Garcia-Ibilcieta D., Sengupta-Gopalan C.;
"Characterization of PII (GLNB) in alfalfa.";
"Characterization of PII (GLNB) in alfalfa.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ database
EMBL; AY027892; AAK16221.1; -.
HSSP; P38504; IGNK.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization;
InterPro; IPR002187; PII_glnB.
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InterPro; IPRuvz...
InterPro; IPRuvz...
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
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Last annotation update ()
P-II.
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Last annotation updat
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larity 85.0%; Pred. No. 5.5e-41;
Conservative 10; Mismatches 7.
 ore 509; DB 10;
ed. No. 7.1e-43;
Mismatches 7
                                                                                                                                                                                                                                                                                                                       194 AA
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   Score
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SEQUENCE FROM N.A.
MEDLINE=22825698; PubMed=12917642;
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il Similarity 90.3%;
102; Conservative
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Best Local S
Matches 64
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QBDLAS;
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chaïn P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M. Shaw S.L., Steglich C., Sullivar W.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.; "Genome divergence in two Prochlorococcus ecotypes reflects oceaniche differentiation.";
                                                                                                                                                                                                            112
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Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
EMBL; AJ251822; CAB75358.1; -.
EMBL; AP2095; AH2095.
HSSP; P05826; 2PII.
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rint
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=PCC 7120;
Gonzalez L., Phalip V., Zhang C.C.;
"Phosphorylation of the signal transduction protein PII by kinase PknC in the cyanobacterium Anabaena sp. strain PCC 7 Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEA.
                                                                                                                                                                                                                                                                                                                                                     Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                 Indels
                                                                                                       SCA64D6663ED3B65 CRC64;
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GO:0006808; P:regulation of nitrogen utilization;
                                                                                                                          16;
                                                                                                                                                                                                                                                                                                             1. 15, Last sequence update)
1. 25, Last annotation update regulatory protein P-II).
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                                                                                                                           322.5; DB 1
No. 1.5e-24;
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No. 3.8e-24;
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MEDLINE=21595285; PubMed=11759840;
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IPR002332; PII GlnB UMP
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I_GLNB_UMP; 1
                                                                                                                                               21;
                                                                                                       12362 MW;
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ProDom; PD001194; PII glnB; 1.
PRCSITE; PS00638; PII GLNB CTE
PRCSITE; PS00496; PII GLNB UMP
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(TrEMBLrel. 25, I
(Nitrogen require
                                                                                                                         57.5%;
                                                                      BX572099; CAE21656.1;
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                                                                                                                                               Conservative
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543; P-II;
                                                                                                      112 AA;
                                                                                                                                    Similarity
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112 AA;
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01-0CT-2000
01-0CT-2003
                                                                                                                                             64 ;
                                                                                                                         Query Match
Best Local S
Matches 64
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                                                                                                                                                                                                           63
                                                                                                     SEQUENCE
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Pfam; PF0
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                                                                        Nature
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                               KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRHGGSEFSEDKFVAKVKM
                                                 KVEAIVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
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Ira T., Kishida Y.,
10 A., Nakazaki N.,
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."; DNA Res. 9:123-130{2002}.

EMBL; AP005370; BAC08143.1; -. GO: GO:0030234; F:enzyme regulator activity; IEA. GO: GO:0006808; P:regulation of nitrogen utilization; IEA.
                                                                                              EIVVKKDQVESVINTIIEGARTGEIGDGKIFVLPVSDVIRVRTGERGEKA
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P-II.
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Mismatches
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                                                                                                                                                                                                                                                     Created)
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PROSITE; PS00638; PII GLNB CTER;
PROSITE; PS00496; PII GLNB UMP;
24;
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InterPro; IPR002332; PII GlnB |
Pfam; PF00543; P-II; 1.
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larity 58.2%;
Conservative 22
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Conservative
                                                                                                                                                                                                                                                                                                                                  Synechococcus elongatus
Bacteria, Cyanobacteria,
NCBI_TaxID=32046;
                                                                                                                                                                                                                    PRELIMINARY;
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Synechococcus sp. (strain Bacteria; Cyanobacteria; NCBI_TaxID=32049;
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64; Conserv
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SEQUENCE 112 AA;
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Matches 61
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SEQUENCE FROM N.A.
STRAIN=Z2491 / Serogroup A / Serotype 4A;
STRAIN=Z2491 / Serogroup A / Serotype 4A;
MEDLINE=20222556; PubMed=10761919;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Klee S.R., Morelli G., Basham D., Peltwell T., Hamlin N., Holroyd Davies R.M., Davis P., Devlin K., Peltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
meningitidis Z2491.";
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                                                                                                                                                                       EMBL; AF120107; AAF63031.1; --
HSSP; P05826; 2PII.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII glnB.
InterPro; IPR00232; PII glnB.
InterPro; IPR00232; PII glnB.
PF131; 1.
PROM; PR001194; PII glnB. 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00638; PII GLNB UMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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EMBL; AL162753; CABB3744.1; -.

PIR; H81961; H81961.

HSSP; P05826; 2PII.

GO; GO:00006808; P:regulation of nitrogen utilization; IEA.

InterPro; IPR002187; PII glnB.

InterPro; IPR002332; PII GlnB_UMP_S.

Pfam; PF00543; P-II; 1.
                                                                                                    Synechococcus
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Pred. No. 6.1e-24;
7; Mismatches 22
                                                                            T., Bryant D.A.; of glnB and bcp genes in
                                                                                                                                                          the EMBL/GenBank/DDBJ
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PII GLNB CTER;
PII GLNB UMP; 1
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                                                                                                                "Nucleotide sequence
                                                                                                                                                                     (JAN-1999)
                                                                                  Gruber
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                             FROM N.A
                               SEQUENCE FROM 1
STRAIN=PCC7002
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                                                                                                                          STRAIN=MCS6 FROM N.A.

STRAIN=MCS6 / Serogroup B;

STRAIN=MCS6 / Serogroup B;

MEDLINE=20175755; PubMed=10710307;

MEDLINE=20175755; PubMed=10710307;

MEDLINE=20175755; PubMed=10710307;

A Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.

A sisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

A Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Mason T., Ciecko A., Masignani V., Pizza M., Grandi G., Sun L.,

Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

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Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;

Science 287:1809-1815{2000}.

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Last annotation update)
P-II.
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No. 4.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
                                                24 ;
55.0%; Score 308.5; DB 55.5%; Pred. No. 3.8e-23.ive 24; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 AA
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Pred. No. 4.8e-
                                                                                                                                                                                                                                                                                                                                                                                                         Z
                                                                                                                                                                                                                                                                                                                                                                                                        112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (serogroup B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
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PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00638; PII GLNB CTER;

PROSITE; PS00496; PII GLNB UMP; 1
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                                                      24;
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15,
25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseriaceae, Neisseria.
NCBI_TaxID=491;
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
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60; Conserva
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3 KVEALVRPWRIQQVSSALLKIGIRGVTVSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKM
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Palinska K.A., Loiseaux-de Goer S., Blondel A., Castets A.M.,
Rippka R., Tandeau de Marsac N.;
"In spite of synthesizing a cyanobacterial-type PII protein, the
oceanic photosynthetic prokaryote Prochlorococcus marinus, strai
9511, is unable to utilize nitrate.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RMBL; AJZ71089; CAB87556.1; -.
HSSP; P38504; IGNK.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII glnB.
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; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castets A.M.,
                                                                                                                                                                                                                                                                                                                                   Prochlorococcus sp. (strain PCC 9511).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcacee Prochlorococcus.
NCBI_TaxID=100363;
Length
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IW; 42B3497E6B4472CD CRC64;
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Last annotation update)
P-II.
                                                                                                                                                                                                            (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.1%; Score 303.5; DB 2; larity 52.7%; Pred. No. 1.2e-22; Conservative 27; Mismatches 24;
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NCBI_TaxID=59919;
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                                                                                                                                                                                                           Created)
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Probom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTE
SEQUENCE 112 AA; 12314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, Nitrogen regulatory protein
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                                                                                                                                                             PRELIMINARY
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nes 58; Conser
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                                                                                                                                                                                                                                                                                           GlnB protein.
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01-OCT-2000
01-OCT-2000
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Q7V025;
01-0CT-2003
                                     62
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Matches
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                                                                                                                            Bacteria; protechacteria; Alphaproteobacter diazotrophicus].
Acetobacteraceae; Gluconacetobacter.
NCBI_TaxID=33896;
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Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales;
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112
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Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur
Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AE017151; AAP95074.1; -.
                                                                                                                                                                                                                                                                                                                                               Perlova O., Meletzus D.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF318039; AAN59757.1; -.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; II
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB UMP S.
Pfam; PF00543; P-II; 1.
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52AB6F9C0CC8D124 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative nitrogen regulatory protein P-II.
                                          Created)
Last sequence update)
Last annotation update)
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Pred. No. 9.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h Similarity 52.7%; Score 305.5; DB 2; Similarity 52.7%; Pred. No. 7.6e-23; 58; Conservative 25; Mismatches 26;
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PRODOM; PD001194; PII glnB; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

SEQUENCE 112 AA; 12431 MW; 52AB
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                                                23,
23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                             (TrEMBLrel.
(TrEMBLrel.
                                                                                                                      Regulatory protein PII GLNB.
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SEQUENCE 112 AA
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01-OCT-2003
01-OCT-2003
01-OCT-2003
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                                                                   01-MAR-2003
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                                                  01-MAR-2003
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MEDLINE 22735913; PubMed = 12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellula
strain 1.";
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Bacteria, Cyanobacteria, Prochlorophytes, Prochlorococcaceae;
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein PII.
GLNK OR PRO1616.
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EMBL; BX294138; CAD72936.1; -.
Complete proteome.
SEQUENCE 133 AA; 14941 MW; 05D489DB4D7B169D C
                                                               16;
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein P-II.
GLNB OR RB2975.
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Pred. No. 2.4e-22;
7; Mismatches 22;
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Pred. No. 1.2e-22
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larity 52.7%;
Conservative
     Nature 424:1042-1047(2003).
EMBL; BX572094; CAE19922.1;
Complete proteome.
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RC STRAIN=SARG / CCMP 1375 / SS120;

RX MEDLINE=22810154; PubMed=12917486;
RA Duffresne A., Salamoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA Barbe V., Duprat S., Galperin M.Y., Koonin B.V., Le Gall F.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
RA Scanlan D.J., Tandeau S.J., Radovo660.1; -.
RA Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT a nearly minimal Dayphoctoriophic genome.";
RA Complete proteome.
SEGUENCE 112 AA, 12239 MW; 3c4E9F51F49806EF CRC64;
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SEGUENCE 112 AA, 12239 MW; 3c4E9F51F49806EF CRC64;
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Scoring table:

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# ALIGNMENTS

RESULT 1

Z 113 AAB69496 standard; protein;

AAB69496;

entry) (first 23-APR-2001

Ricinus communis PII protein.

bean; PII; plant nitrogen regulatory gene; P-PII; en assimilation; transgenic plant; herbicide screening Castor be 

Ricinus communis.

US6177275-B1

23-JAN-2001.

97US-00899330. 23-JUL-1997; 96US-0022328P 24-JUL-1996;

(UYNY ) UNIV NEW YORK STATE.

Hsieh M; Lam H, G. M. Coruzzi

AAF58584. WPI; 2001-158572/16 N-PSDB; AAF58582, A Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 1; Fig 1; 35pp; English.

The present sequence is encoded by a nitrogen regulatory PII gene. Movel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

Sequence 113 AA;

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Novel P-PII
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                                                                                                                                                                    Synechococcus; PII; plant nitrogen regulatory gene; nitrogen assimilation; transgenic plant; herbicide
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Pred. No. 4.2e-28
L; Mismatches 2
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                                                                                                                             PII
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AAB69503 standard; protein; 112
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Conservative 21;
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62; Conse
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                                                                                                                              Synechococcus
                                                                                                                                                                                                                                        Synechococcus
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gene. Novel
isolated.
                                                                                                          The present sequence is encoded by a nitrogen regulatory PII gene. Nove plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clorwith the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRQGGSEFSEDKFVAKVKM
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                        and as probes for isolation, gene promoters.
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for isolating
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29.;
                                    of regulating plant
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Pred. No. 3.8e-2
5; Mismatches
                                               transgenic plant production, genomic clones having P-PII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                     P-PII
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Pred. No. 1.1e-27;
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ilarity 54.5%;
Conservative 25
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gonorrhoeae
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                                                                                                                                                                                                                                                           Disclosure; Page
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                                                                                                     12-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is encoded by a nitrogen regulatory PII gene. plant PII (also called P-PII) nucleotide sequences have been isolat They are useful for regulating nitrogen assimilation in plants, and transgenic plant production. They are also used to engineer organis that overexpress wild-type or mutant P-PII regulatory proteins. P-P proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic with the promoters of P-PII genes. P-PII promoters are light- and/o sucrose-inducible, and are suitable for genetic engineering of plan
transgenic plant production. They are also used to engineer organis that overexpress wild-type or mutant P-PII regulatory proteins. P-P proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic with the promoters of P-PII genes. P-PII promoters are light- and/o sucrose-inducible, and are suitable for genetic engineering of plan
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                                                                                                                         DB 4.;
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Pred. No. 1.5e-24;
5; Mismatches 28;
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larity 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                      <del>=</del>1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, measuring expression of a gene, analyzing or pattern of a gene and identifying homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yokoi
                                                                                                                                                                                                                                           saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + Sequence Listing; English.
                                                             BIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacteria,
                                                                                                                                                                                                                                          synthesis; vitamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Hayashi M,
Ozaki A;
                                                                                                                                                                                                                  6980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.6%; Score 270.5;
larity 45.0%; Pred. No. 7.5e
Conservative 33; Mismatches
                                                                                                                                                                                                                  SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from mutation point of a gene, measuring expression profile or pattern of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                           acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          H, Ando
Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246pp
                                                                                                                                         112
                                                                                                                                                                                                                   fragment
                                                                                                                                                                                                                                                                                                                                                                                 99JP-00377484.
2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                     (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                          2000EP-00127688
                                                                                                                                                                                                                                              amino
                                                                                                                                         standard; protein;
                                                                                                                                                                                                                                                                               glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 6980;
                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mizoguchi
Senoh A,
                                                                                                                                                                                                                                                        acid synthesis.
                                                                                                                                                                                                                     glutamicum protein
                                                                                                                                                                                                                                              bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-376931/40.
N-PSDB; AAH68445.
                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 112 AA;
                                                                                                                                                                                                                                                                                  Corynebacterium
                                                                                                                                                                                                                                                                                                           EP1108790-A2.
                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1999;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
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                                                                                                                                                                                           26-SEP-2001
                                                                                                                                                                                                                                                                                                                                   20-JUN-2001
                                                                                                                                                                                                                                              Coryneform
                                                                                                                                                                  AAG93226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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Best Local
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Matches
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Gaps

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Indels

Length 112;

Score 274.5; DB 4; Pred. No. 2.5e-24;

25;

49.3%; larity 50.0%; Conservative

Similarity 55; Conser

Query Match Best Local S Matches 55

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Rhodobacter capsulatus PII protein.
                                                                                                                  96US-0022328P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00899330
                                                                                                                                    (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium leguminosarum PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium leguminosarum.
                 Rhodobacter capsulatus;
nitrogen assimilation;
                                           capsulatus
                                                                                                                                                      Lam H,
                                                                                                                                                                       2001-158572/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                       A.
                                                             US6177275-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6177275-B1.
                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                  24-JUL-1996;
                                                                                                 23-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1997;
                                            Rhodobacter
                                                                                                                                                      ₽
                                                                               23-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                 useful for additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB69499;
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69499
                                                                                                                                                      Coruzzi
                                                                                                                                                                                         Novel
                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                                                                                                                                                                                     reagents
                                                                                                                                                                                                                                                                                                                     pents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated Acinetobacter baumannii nucleic acids The A. baumannii rucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEALLRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                  Acinetobacter baumanii proteins and nucleic acids, useful as
diagnosing a bacterial disease, as components of antibacteria
sines, as targets for antibacterial drugs, or as biocontrol ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **
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111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 124;
63 VIISDAQAEEVINIIVETARTGKVGDGKVMMTNIEELVRVRTGERGEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVVSKDQVEDVIEKLIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 256.5; DB 6
Pred. No. 3.8e-22;
2; Mismatches 33
                                                                                                                   disease;
                                                                                                                                                                                                                                                                                                                                               Example; SEQ ID NO 5437; 328pp; English
                                                                                                 Acinetobacter baumannii protein #1311
                                                                                                                    bacterial
                                                                                                                                                                                                                                      CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 112
                                             124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                   99US-00328352
                                                                                                                                                                                                                    98US-0088701P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.18;
                                             protein;
                                                                                                                                                                                                                                    THERAPEUTICS
                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                    panmanni;
                                                                                                                                              baumannii
                                                                                                                           plant biocontrol agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                               (first
                                             standard;
                                                                                                                                                                                                                                                       Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                 N-PSDB; ADA30024
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                      GENOME
                                                                                                                                              Acinetobacter
                                                                                                                   Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                   18661-NUL-60
                                                                                                                                                                US6562958-B1
                                                                                                                                                                                                   04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2001
                                                                               20-NOV-2003
                                                                                                                                                                                3-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                               plants, The baumannii
                                                                                                                                                                                                                                                                                                                     vaccines,
                                                                                                                                                                                                                                                                        2003
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Best Local S
Matches 53
                                                              ADA34150;
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                                             ADA34150
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                                                                                                                                                                                                                                     (GENO-)
                                                                                                                                                                                                                                                        Breton
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                                    ADA341
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regulatory PII gene. Novel suces have been isolated.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KVBAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KVEALIKPFKLDBVKBALQEAGIQGLSVIEVKGFGRQKGHTELYRGAEYVVD-FLPKVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ssimilation,
for isolating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112;
PII; plant nitrogen regulatory gene; transgenic plant; herbicide screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIVVSKOQVEDVIEKIIBEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PII genes capable of regulating plant nitrogen I for transgenic plant production, and as probes fional genomic clones having P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.9%; Score 255.5; DB 4;
larity 47.3%; Pred. No. 4.4e-22;
Conservative 26; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
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Gaps

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Indels

1.; 29;

Score 248; DB 4; Pred. No. 3.4e-21 5; Mismatches 2

26;

Similarity 46.7%; 50; Conservative 2

Query Match Local

503

Matches

Best

Sequence 111 AA;

Length 111;

9

109

|:|||::|:::::|| | :||::||::||| | | : |:||: 3 KIBAIIKPFKLDEVRS-LSGVGLQGITVTEAKGFGRQKGHTDLYRGABYIVD-FLPKVKI 3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM

EIVVSKDQVEDVIEKTIEEARTGEIGDGKIFLLPVSDVIRVRTGERG

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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

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The present sequence is encoded by a nitrogen regulatory PII gene. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PII;
                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                             of regulating plant nitrogen assimilatint production, and as probes for isolatinaving P-PII gene promoters.
                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        im; PII; plant nitrogen regulatory gene
transgenic plant; herbicide screening.
                                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                                                                                                                                           107
                                                                                                                                                                                                                                                                                                                     111;
                                                                                                                                                                                                                                                                                                                                                                                                                    EIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERG
                                                                                                                                                                                                                                                                                                                                                                                                                               ENTRADENARAVIBATRKAAQTGRIGDGKIEVSNVEEVIRIRTGETG
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                     Score 251; DB 4; I
Pred. No. 1.5e-21;
7; Mismatches 27;
                                                                                                          useful for transgenic plant production, additional genomic clones having P-PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bradyrhizobium japonicum PII protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111
                                                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                Example; Fig 1; 35pp; English
                                                                                                                                                                                                                                                                                                                     45.1%;
larity 47.7%;
Conservative 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-00899330
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96US-0022328P
                        (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein;
                                                Hsieh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sobium japonicum;
assimilation; tra
                                                                                              genes capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                              Lam H,
                                                                       2001-158572/16
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium
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(II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                           forensic;
                                                                                                                                                                                                                         1; chromosome mapping; gene mapping; gene therapy; forensisupplement; medical imaging; diagnostic; genetic disorder
            107
|||: | || ||: || || ||| |||||||| || EIVIGDDLVBRAIDAIRRAAQTGRIGDGKIFVSNIEEAIRIRTGESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 54613; 103pp; English.
                                                                                                                                                                                                Novel human diagnostic protein #24245.
                                                                                              160
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2000US-00649167
                                                                                                ABG24254 standard; protein;
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23-AUG-2000;
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                                                                                                                                ABG24254;
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I genes capable of regulating plant nitrogen assimilat transgenic plant production, and as probes for isolat genomic clones having P-PII gene promoters.

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Hsieh

Lam H,

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WPI; 2001-158572/16

Novel P-PII

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Fig 1; 35pp; English

Example:

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supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Noter the convertion of the convertion of the convertion of the convertion of the convertion.
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                                                                                                                                                                                                                                                 Gaps
                                                                                                                    amino acid sequences of the invention. Note: The sequence data for patent did not appear in the printed specification, but was obtained electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum, homeostasis, adaptation, HA protein, fine chemical production, organic acid, proteinogenic amino acid, nonproteinogenic amino acid, purine base, pyrimidine base, nucleonucinostide, lipid, saturated fatty acid, unsaturated fatty acid, carbohydrate, aromatic compound, vitamin, cofactor, polyketide; elaphosis, Corynebacterium diphtheriae, genetic engineering, Brevibacterium, environmental condition.
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                                                                                                                                                                                                                    Score 245.5; DB 'Pred. No. 1.1e-20
); Mismatches 3(
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99DE-01031636.
99DE-01032126.
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AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. glutamicum HA genes (I) can be used in vectors for expression in host cells and production of fine chemicals, such as, an organic acid, cells and production of fine chemicals, such as, an organic acid, proteinogenic or nonproteinogenic amino acid (preferred), purine or pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, collyketide or enzyme. The amino acids produced can be lysine, glutamine, collyketide or enzyme. The amino acids produced can be lysine, glutamine, cysteine, valine, leucine, isoleucine, serine, threonine, methionine, tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for glutamicum genome or can be used as markers for genetically engineered Corynebacterium or Brevibacterium. The HA proteins encoded by the (I) are used to maintain homeostasis in C. glutamicum or help the microorganism to adapt to different environmental
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Pred. No. 2e-20;
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99DE-01041390.
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(first en
                                                                                                                       Kroeger
                                                                                                                                                                                                                                                      Page 563;
                                                                                                                                               2001-061974/07
B; AAF71296.
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14-JUL-1999;
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16-MAY-2002
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                  New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                              Ehrlich SD;
                                                                                                                                                                                                                                                             SEQ ID NO 1639; 2504pp; French.
                                                                                          INST NAT RECH AGRONOMIQUE
                                                                                                                              Renault P,
                                                     2000FR-00004630
                     11-APR-2000; 2000FR-00004630
                                                                                                                               Sorokine A,
                                                                                                                                                                  WPI; 2002-043418/06.
                                                                                             (INRG ) INRA
                                                      11-APR-2000;
                                                                                                                               Bolotine A,
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Sequence 112 AA;

2 3 KVEAILRPWRVSQVSSALLKIG-IRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVK 61 61 |:|||:| : : :|| | :||| | ::|:| 3 KIEAIIRTDKLEDLKAALSDNGLVHGMTVSQVLGYGEQKGFTBYVRGQRI-ETTLLSKLK Gaps Length 112; 39.1%; Score 218; DB 5; 1 llarity 43.2%; Pred. No. 1.2e-17; Conservative 24; Mismatches 37; Query Match Best Local Similarity g ਨੇ

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2004, 19:13:03 Search completed: May 24, Job time: 52 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                 Copyright
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model ¥. O using protein search, OM protein 2004, 19:10:08 ; Search time 14 Seconds May 24, on: Run

(without alignments) 776.403 Million cell

ss/sec update

JS-09-756-541-2 557 1 FYKVEAILRPWRUS score: Title: Perfect

..LLPVSDVIRVRTGERGDKAE FYKVEAILRPWRVSQVSSAL. Sequence:

Gapext BLOSUM62 Gapop 10.0 Scoring table:

283366 seqs, 96191526 residues Searched:

0

283366 ij number Total

hits satisfying chosen parameters

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4 0 6 4 . . . . . .

pir4:\*

inted, Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pri and is derived by analysis of the total score distribution.

# STIMMARIES

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## ALIGNMENTS

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C; Species: Arabidopsis thaliana (mouse-ear cress)

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C; Date: 10-Feb-2001 #sequence_revision 16-Feb-2001

C; Date: 10-Feb-2001 #sequence_revision 16-Feb-2001

C; Date: 10-Feb-2001 #sequence_revision 16-Feb-2001

R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp.

A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A; Reference number: A85001; MUID:20083488; PMID:10617198

A; Reference revision: A; Coss-references: GB:NC_001268; NID:97268574; PIDM:CAB80683.1; GSPDB:GN00140

C; Genetics:

A; Map position: 4
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nitrogen regulatory protein P-II glnB [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. pcC 7120
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002
C;Accession: AH2095
C;Accession: AH2095
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 2:55-213, 2:001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUD: 21595285; PMID: 11759840
A;Residues: 1-112 < KUR>
A;Residues: 1-112 < KUR>
A;Residues: 1-112 < KUR>
A;Residues: 1-112 < KUR>
A;Exosi-references: GB:BA000019; PIDN: BAB74018.1; PID: G17131411; GSPDB: GN00179
A;Exosi-mental source: strain PCC 7120
C;Genetics:
A;Genetics:
A;Genetics:

Best Loc Matches

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nitrogen regulatory protein p-II NWB1995 [similarity] - Neisseria meningitidis (strain l C; Species: Neisseria meningitidis
C; Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Date: 11-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C; Date: 11-Mar-2001
C; Date: 11
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A;Variety: PCC 7942; PCC 6301

C;Species: Synechococcus sp.

A;Variety: PCC 7942; PCC 6301

C;Date: 08-Nov-1991 #text_change 26-Aug-1999

C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 26-Aug-1999

C;Accession: A39696; P56817

R;Tsinoremas, N.F.; Castets, A.M.; Harrison, M.A.; Allen, J.F.; Tandeau de Marsac, N. Proc. Natl. Acad. Sci. U.S.A. 88, 4565-4569, 1991

A;Title: Photosynthetic electron transport controls nitrogen assimilation in cyanobacte: A;Reference number: A39696; MUID:91271233; PMID:1905010

A;Accession: A39696

A;Accession: A39696

A;Residues: 1-112 <TSI>
A;Residues: 1-112 <TSI>
A;Residues: 1-112 <TSI>
A;Residues: 1-12 <TSI>
A;Residues: 1-12 <TSI>
A;Residues: 1-12 <TSI
A;Residues: 1-13 <TSI
A;Residues: 1-14 <TSI
A;Residues: 1-15 <TSI
A;Residues: 1-16 <TSI
A;Residues: 1-17 <TSI
A;Residues: 1-18 <TSI
A;Residues: 10-19 <TSI
A;Residues: 10-19 <TSI
A;Residues: 10-19 <TSI
A;Residue
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            ore 303.5; DB ed. No. 3.5e-21 Mismatches 2
                  DB
                  Score
Pred.
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A;Gene: NMB1995
C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein
F;51/Binding site: UMP (Tyr) (covalent)
                                                                             25;
            54.5%;
illarity 54.5%;
Conservative 2
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Best Local Similarity
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis ; A;Steference number: A81775; MUID:2022556; PMID:10761919
A;Accession: H81961
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83744.1; PID:C;Genetics:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: glnB; NMA0447
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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex a A;Title: The complete genome of the hyperthermophilic bacterium Aquifex a A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Reference number: A70310
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Reference number: A70310
A;Residues: 1-112 <AQF>
A;Residues: 1-112 <AQF>
A;Residues: 1-112 <AQF>
A;Cross-references: GB:AE000674; NID:g2982850; PIDN:AAC06473.1; PID:g2982
A;Experimental source: strain VF5
C;Genetics:
A;Gene: glnB
C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein; signal transduction
F;51/Binding site: UMP (Tyr) (covalent) #status predicted
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change
C;Accession: F70310
R;Deckert, G.; Warren, P.V.; Gaasterland, T. v...
V.
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C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein
F;51/Binding site: UMP (Tyr) (covalent) #status predicted
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larity 53.6%; Pred. No. 3.4e-22;
Conservative 29; Mismatches 21;
                                                           Score 315.5; DB 2;
Pred. No. 2.7e-22;
2; Mismatches 23;
P-II
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Similarity 58.2%; Prof
64; Conservative 22;
 C; Superfamily: regulatory protein
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nitrogen regulatory protein P-II [similarity] - Vibrio cholerae [strain N1696i serogroup C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 24-Aug-2001
C; Accession: D82102
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, Pl. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
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Dougan, G.;
S.; Barrell,
                                                                                                                                                                                                                                            1995
                                    genome
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C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C; Accession: AF0354
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C; Accession: AF0354
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentideno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Doug deno-Tarraga, A.M.; Simmonds, M.; Skelton, J.; Stevens, R.Y.; Whitehead, S.; E Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Accession: AF0354
A; Residues: Dreliminary
A; Molecule type: DNA
A; Residues: 1-112 < KURx>
A; Cross-references: GB:AL590842; PIDN:CAC92161.1; PID:g15980875; GSPDB:GN00175
C; Genetics:
A; Gene: glnB
C; Superfamily: regulatory protein P-II
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1arity 52.7%; Score 278.5; DB 2
Conservative 21; Mismatches 30
Plant Mol. Biol. Rep. 13, 333-335, 1995
A; Title: Complete nucleotide sequence of the Porphy A; Reference number: S73108
A; Accession: S73175
A; Accession: S73175
A; Molecule type: DNA
A; Regidues: 1-112 < REI>
A; Regidues: 1-112 < REI>
A; Cross-references: EMBL: U38804; NID:g1276652; PIDPA; Experimental source: strain Avonport
A; Conetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: regulatory protein P-II
C; Keywords: chloroplast; phosphoprotein; signal tre
F; 51/ Binding site: UMP (Tyr) (covalent) #status pre
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$13078

nitrogen regulatory protein P-II - Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 26-3
C;Accession: $13078
R;de Zamaroczy, M.; Delorme, F.; Elmerich, C.
Mol. Gen. Genet. 224, 421-430, 1990
A;Title: Characterization of three different nitrogen-regulated pror
A;Reference number: $13078; MUID:91094780; PMID:1702507
A;Accession: $13078
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A; Note: modification state depends on the nitrogen source
C; Superfamily: regulatory protein P-II
C; Keywords: phosphoprotein; signal transduction
E; 49/Binding site: phosphate (Ser) (covalent) #status pred
F; 51/Binding site: UMP (Tyr) (covalent) #status predicted
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nitrogen regulatory protein P-II - red alga (Porphyra pur
C;Species: chloroplast Porphyra purpurea
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_
C;Accession: S73175
                number: A56817; MUID:91355213; PMID:1653017
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larity 49.1%; Pred. No. 3.8e-19;
Conservative 26; Mismatches 29;
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                                                                                             type: protein: 1-40 <Li1>
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             A; Reference number: A56
A; Accession: F56817
A; Status: preliminary
A; Molecule type: protei
A; Residues: 1-40 <LII>A; Experimental source: C; Genetics:
A; Genetics:
A; Gene: glnB
C; Function:
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the uridylylated form of P-II forms a complex with nitrogen regulation protein II A; Note: phosphorylated nitrogen regulation protein I (ntrC) activates transcription of 1 C; Function: ATR>
A; Description: uridylylated P-II forms a complex with nitrogen regulation of 1 (ntrC) activates transcription of 1 (y) Description: uridylylated P-II forms a complex with a co
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C;Date: 30-Jun-1988 #sequence revision 10-Nov-1995 #text_change 01-Mar-2002 C;Accession: C49940; S15991; R29307; S3753; H65032; S31961
R;Liu, J; Magasanik, B
J. Batceriol. 175, 7441-7449, 1993
A;Title: The glnB region of the Escherichia coli chromosome.
A;Reference number: A49940; MUID:94042920; PMID:8226691
A;Recession: C49940
A;Residues: 1-112 cLIU
A;Residues: 1-120, ABB-28719; MUID:9455660; PIDN:AAB28779.1; PID:9455663
A;Note: sequence extracted from NCBI backbone (NCBIN:139878; NCBIP:139882)
A;Cross-references: GB:S67014; NID:9455660; PIDN:AAB28779.1; PID:9455663
A;Note: sequence extracted from NCBI backbone (NCBIN:139878; NCBIP:139882)
A;Residues: 1-12 cLIU
A;Reference number: S15991; MUID:91238719; PMID:2034230
A;Accession: S15991
A;Accession: S15991
A;Accession: S15991
A;Accession: S15901
A;Accession: S15901
A;Accession: S2001
A;Accession: A;A
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A;Note: free glutamine synthase is active; adenylylated glutamine
C;Superfamily: regulatory protein P-II
C;Keywords: phosphoprotein; signal transduction
F;51/Binding site: UMP (Tyr) (covalent) #status experiment
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A; Residues: 1-12 < VAN>
A; Residues: 1-12 < VAN>
A; Cross-references: EMBL: Z21843; NID: 949395; PIDN: CAA79890.1;
A; Bxperimental source: strain K-12, substrain W3110
A; Bxperimental source: strain K-12, substrain W3110
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12
A; Title: The complete genome sequence of Escherichia coli K-12
A; Reference number: A64720; MUID: 97426617; PMID: 9278503
A; Accession: H65032
A; Accession: H65032
A; Status: nucleic acid sequence not shown; translation not shown; A; Molecule type: DNA
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A; Residues: 1-18, 'R', 20-80, 'E', 83-102, 'VP' <SON>
A; Residues: 1-18, 'R', 20-80, 'E', 83-102, 'VP' <SON>
A; Cross-references: GB: M16778; NID: g146165; PIDN: AA23883.1;
R; van Heeswijk, W.C.; Rabenberg, M.; Westerhoff, H.V.; Kahn, Mol. Microbiol. 9, 443-457, 1993
A; Title: The genes of the glutamine synthetase adenylylation A; Reference number: S36254; MUID: 94018640; PMID: 8412694
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A;Residues: 1-112 <BLAT>
A;Cross-references: GB:AE000341; GB:U00096; NID:g1788899;
A;Experimental source: strain K-12, substrain MG1655
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A; Status: preliminary
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CrFunction: 
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source: strain M5a1
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                          Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pat A; Reference number: A82035, MUID:20406833; PMID:10952301
A; Reference number: A82035, MUID:20406833; PMID:10952301
A; Reference number: A82035, MUID:20406833; PMID:10952301
A; Reference number: A; Reference number: A; Residues: 1-114 < HEI>
A; Cross-references: GB:AE004295; GB:AE003852; NID:99656789; A; Experimental source: serogroup O1; strain N16961; biotype C; Genetics:
A; Genetics:
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A; Genetics:
C; Genetics:
C; Guperfamily: regulatory protein P-II
C; Superfamily: regulatory protein P-II
C; Superfamily: regulatory protein P-II
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C; Superfamily: sequlatory protein F-II
C; Superfamily: sequlatory protein F-II
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Ol; strain N16961; biotype
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C;Species: Klebsiella pneumoniae
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_C
C;Accession: 504377
R;Holtel, A.; Merrick, M.
Mol. Gen. Genet. 215, 134-138, 1988
A;Title: Identification of the Klebsiella pneumoniae glnB
A;Reference number: 504376; MUID:89201233; PMID:2907369
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C; Keywords: phosphoprotein; signal transduction
F; 51/Binding site: UMP (Tyr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-II indirectly controls the transcription of
see events are reversed
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No. 1,1e-18;
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A, Residues: 1-112 <HOL>
A, Cross-references: EMBL:X14012
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A;Accession: S04377
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A.Gene: glnB
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- Escherichia coli (strain K-12)

nitrogen regulatory protein P-II.1 C;Species: Escherichia coli

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Exportetical protein glnB [imported] - Escherichia coli (strain O157:H7, substra C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: G85900
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: B85900
A; Status: preliminary
A; Molecule type: DNA
A; Experimental source: Strain O157:H7, substrain EDL933
C; Genetics:
A; Gene
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[larity 50.0%; Pred. No. 1.7e-18;
Conservative 25; Mismatches 25
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ANOte: this species has also been called Salmonella typhi

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C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AH0826

C;Accession: AH0826

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;thle: Complete genome sequence of a multiple drug resistant Salmonella enterica servo A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Residues: 1-112 cPAR>
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Pred. No. 1.7e-18;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model procein search, OM protein May 24, 2004, 19:06:17 Run on:

; Search time 10.5 Seconds
 (without alignments)
 560.374 Million cell updates/sec

US-09-756-541-2 557 1 FYKVEAILRPWRVSQVSSAL.

113

.....LLPVSDVIRVRTGERGDKAE

BLOSUM62 Gapop 10.0 , Gapext table: Title: Perfect so Sequence: Scoring

score:

141681 seqs, 52070155 residues Searched:

0.5

141681 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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9	86	<del>.</del>	112	-	GLNB_PASMU	cjkl pasteurel
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8	α,	50.0	112	<b>,</b> -4	GLANB PORPU	1254 porphyra
O1	96.	6	112	Н	GLNB_KLEOX	klebsiella
10	74.	9.	112	Н	GLNB_ECOLI	
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17	60.	s.	112	Н	GLNB_BRAJA	
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24	Δ.	4.	$\vdash$	<b>~</b>	GLNK_ECOLI	8504
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28	81.	2	123	Н	GLN2 METBA	54809
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### ALIGNMENTS

Score 315.5; DB 1; Pred. No. 1e-22;

56.6%; 58.2%;

Query Match Best Local Similarity

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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration
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                                            61
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-! FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN
TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP. P.
II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS),
THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-II
IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS (BY
                      3 KVEAILREWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSBFSEDKFVAKVKM
                                    1 TO
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   Gaps
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                                                                                                                                                                                                                                                                                        STEAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
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                                                                               63 EIVVSKDQVEDVIEKIIEEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA
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Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%; Score 314.5; DB 1; larity 53.6%; Pred. No. 1.3e-22; Conservative 29; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitrogen regulatory protein P-II.
     Mismatches
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB_UMP_
Pfam; PF00543; P-II; 1.
     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AE000674; AAC06473.1;
F70310; F70310.
; P05826; 2PII.
     Conservative
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59; Conser
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Matches 59
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       Matches
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the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homotrimer (By similarity).
PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SOURCE AND SPECTRAL
LIGHT QUALITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTBRQGGSBFSBDKFVAKVKM
||||||:||::::| ||: ||:|||:|||:||:||:|::
3 KVBAIIRPFKLDBVKIALVNAGIVGMTVSEVRGFGRQKGQTERYRGSEYTVE-FLQKLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liotenberg S., Castets A.M., Campbell D., Houmard J.,
Tandeau de Marsac N.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS
-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF NR-I TO
GENB (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I
NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY).
-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN
TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS
THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING
THE ENZYME (BY SIMILARITY).
KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKVKM
                                   Gaps
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R HSSP; P05826; 2PII.

R InterPro; IPR002187; PII glnB.

R InterPro; IPR00232; PII glnB.

R Pfam; PF00543; P-II; 1.

R PRINTS; PR00340; PII glnB; 1.

R ProDom; PD001194; PII glnB; 1.

R PROSITE; PS00496; PII GLNB UMP; 1.

R PROSITE; PS00638; PII GLNB UMP; 1.

R PROSITE; PS00638; PII GLNB UMP; 1.

R PROSITE; PS00638; PII GLNB CTER; 1.

R PROSITE; PS00638; PII GLNB CTER; 1.

R PROSITE; PS00638; PII GLNB CTER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyell
NCBI_TaxID=1197;
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EIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVVRIRTGEKNTEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the P(II) protein family
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                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Nitrogen regulatory protein P-II (PII signal
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                                                                                                                                                                                                                                                                                                                                                Okumura S.,
                                                                                                                                                                                                                                                                                                                                                                                             "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136[1996].

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO SHOSPHORYLATED, THESE EVENTS ARE REVERSED (BY SIMILARITY).

-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACTIVATING THE ENZYME (BY SIMILARITY).
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                                                                                                                                                                                                                             the expression
                                                                                                                                                                                                                                                                                                                                                                       X.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima K., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima K., Hirosawa M., Muraki A., Nakazaki N., Naruo K., Okumu
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumu
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda I
                                                                                               transducing protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homotrimer (By similarity).
PTM: PHOSPHORYLATION DEPENDENT ON THE NITROGEN SCURCE AND
LIGHT QUALITY (BY SIMILARITY).
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PROSITE; PS:00496; PII_GLNB_UMP; 1.
PROSITE; PS:00638; PII_GLNB_CTER; 1.
Transcription regulation; Nitrogen fixation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restric
                                                                                                                                                                                                                          transport control the in the cyanobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (PROBABLE) F9ABD0F5C173B799 CRC64;
                                                                                                                                        Chroococcales; Synechocystis
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                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitrogen regulatory protein P-II (PII signal
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                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98088000; PubMed=9426594;
Garcia-Dominguez M., Florencio F.J.,
"Nitrogen availability and electron
of glnB gene (encoding PII protein)
Synechocystis sp. PCC 6803.";
Plant Mol. Biol. 35:723-734(1997).
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BAA18533.1; ALT_INIT
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InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_
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                                                                                                                                           Cyanobacteria;
                          STANDARD;
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EMBL; D90915;
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                                                                                                                                                          TaxID=1
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                           SYNY3
                                                                                                                                           Bacteria;
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"Phosphorylation of the PII protein (glnB gene product) in the cyanobacterium Synechococcus sp. strain PCC 7942: analysis of in vitro kinase activity.";
J. Bacteriol, 177:5812-5817(1995).
-! FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsinoremas N.F., Castets A.M., Harrison M.A., Allen J.F.,
Tandeau de Marsac N.;
"Photosynthetic electron transport controls nitrogen assimilation
cyanobacteria by means of posttranslational modification of the g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transducing protein)
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STRAIN=PCC 6301;

MEDLINE=90249505; PubMed=2110911;

Harrison M.A., Keen J.N., Findlay J.B.C., Allen J.F.;

"Modification of a glnB-like gene product by photosynthetic transport in the cyanobacterium Synechococcus 6301.";

FEBS Lett. 264:25-28(1990).
                                                                                                                                                               EIVVSKDQVEDVIEKIIEEARTGEIGDGKIFLLPVSDVIRVRTGERGDKA
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Forchhammer K., Tandeau de Marsac N.;
"The PII protein in the cyanobacterium Synechococcus si
7942 is modified by serine phosphorylation and signals
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SEQUENCE OF 1-40.
STRAIN=PCC 6301;
MEDLINE=91355213; PubMed=1653017;
Li N., Warren P.V., Golbeck J.H., Frank G., Zuber H., "Polypeptide composition of the Photosystem I complex Photosystem I core protein from Synechococcus sp. PCC photosystem I core photosystem 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Symechococcus sp. (strain PCC 6301) (Anacystis nidula: Bacteria; Cyanobacteria; Chroococcales; Synechococcus NCBI_TaxID=1140, 1139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A. 88:4565-4569(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogen regulatory protein P-II (PII signal
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MEDLINE=96011366; PubMed=7592328;
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STRAIN=PCC 7942;
MEDLINE=91271233; PubMed=1905010
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J. Bacteriol. 176:84-91(1994)
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Submitted (JUL-1998) to the
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STRAIN=PCC 6301;
Inoue K., Bryant D.A.;
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-1 - FUNCTION: IN NITROGEN-LIMITING
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P21193;
01-MAY-1991 (
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBE outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE - SI145866; PubMed - 11248100;

May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTED TO P-II-UMP, THESE CONVERSION OF NR-I TO NR-I IS URIDYLYLATED TO P-II-UMP, THESE
                          GLN
   P-II
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NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHE IS PHOSPHORYLATED, THESE EVENTS ARE REVERSED. FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO TO 2-KETOGLUTARATE DECREASES, P-II IS PHOSPHORYLATED WHICH THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS), THUS ACT
                                                                                   THE NITROGEN SCURCE AND
                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation
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5F44B64CBFF3C559 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                          SIMILARITY: Belongs to the P(II) protein family.
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InterPro; IPR002332; PII glnB UMP S.
PFam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB UMP; 1.
Transcription regulation; Nitrogen fixation; Pho MOD RES 49 49 PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 306.5; DB 1;
Pred. No. 7.2e-22;
1; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitrogen regulatory protein P-II.
                                                                                      Ö
                                                                                   PIM: PHOSPHORYLATION DEPENDENT
LIGHT QUALITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                           12391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                55.0%;
                                                                                                                                                                                                                              EMBL; M62447; AAA27312.1; -.
EMBL; AF079137; AAF04333.1;
PIR; A39696; A39696.
HSSP; P05826; 2PII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                            : Homotrimer.
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                                                                                                                                                                                                                                                                                                                                                                                                             112 AA;
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                                                                 ENZYME
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16-OCT-2001
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                                                                            SUBUNIT
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Best Local
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ANE, SO ACTIVATING
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de Zamaroczy M., Delorme F., Elmerich C.;
"Characterization of three different nitrogen-regulated promoter regions for the expression of glnB and glnA in Azospirillum brasilense.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azospirillum brasilense.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
TO 2-KETOGLUTARATE , WHICH CAUSES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
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||||::||: || |:||:||:|||||:||
62 EIVVTDEQVDQCIEAIMETAQTGKIGDGKIFVYDVERVIRIRTGEENEDA
       EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTY DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES DEADENYLYLATION OF GLUTAMINE SYNTHETASE BY GLNE, SO ACTIVENZYME (BY SIMILARITY).

SUBUNIT: Homotrimer (By similarity).

PTM: Uridylylated/deuridylylated by glnD (By similarity)

SIMILARITY: Belongs to the P(II) protein family.
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MEDLINE=87076765; PubMed=2878685;
Bozouklian H., Elmerich C.;
"Nucleotide sequence of the Azospirillum brasilense synthetase structural gene.";
Biochimie 68:1181-1187(1986).
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(3)
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52.7%; Pred. No. 5.2e-20;
ive 23; Mismatches 28
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on update)
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01-MAY-1991 (Rel. 18, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
Nitrogen regulatory protein P-II.
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Mol. Gen. Genet. 224:421-430(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006236; AAK04088.1; -. HSSP; P05826; 2PII. InterPro; IPR002187; PII_glnB. InterPro; IPR002332; PII_GlnB_UMP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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SYNTHETASE,
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GLUTAMINE
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PIR; S73175; S731...
HSSP; P05826; 2PII..
InterPro; IPR002187; PII glnB.
ThterPro; IPR002332; PII GlnB_UN
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Bacteria; Proteobacteria; Gamma
Enterobacteriaceae; Klebsiella.
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                                                                                                                                                                                                                                                                                                                          50.0%;
ilarity 52.7%;
Conservative 23
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                        : Homotrimer
                                   SIMILARITY: Belongs
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  DEADENYLYLATION
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58; Conser
             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=571;
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                         SUBUNIT
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GLNB
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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch}.
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                                                             유부
          (GS)
P-II
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   TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP.
P-II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-I IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.
FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GS GENE {GLNA}. P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-I IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED.
SUBBUNIT: Homotrimer (By similarity).
SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALY CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, TH EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARAT DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Avcnport;
Reith M.E., Munholland J.;
"Complete nucleotide sequence of the Porphyra purpurea chloropla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Nitrogen regulatory protein P-II.
                                                                                                                                                                                                                                                                                                                                                                 Transcription regulation; Nitrogen fixation.
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                                                                                                                                                                                                                                                          PIR; $13078; $13078.

HSSP; P05826; 2PII.
InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_S
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGENB.
ProDom; P0001194; PII_glnB; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
PROSITE; PS00496; PII_GLNB_UMP; 1.
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                                                                                                                                           rough a collaboration e EMBL outstation restrictions on it
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P-II
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SO ACTIVATING THE ENZYME
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TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UME
P-II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (
THUS ACTIVATING THE ENZYME. CONVERSERLY, IN NITROGEN EXCESS P-
IS DEURIDYLATED AND PROMOTES THE ADENYLATION OF GS.
FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE G
GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I
NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-
IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE REVERSED.
SUBUNIT: HOMOLrimer (By similarity).
SIMILARITY: Belongs to the P(II) protein family.
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PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

Transcription regulation; Nitrogen fixation; Chloroplast.

Transcription regulation; Nitrogen fixation; Chloroplast.

BINDING 51 51 UMP (BY SIMILARITY).

BINDING 51 5220 MW; 29416AA49FC37AI8 CRC64;
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sequence of wild-type and mutant alleles.";
Mol. Gen. Genet. 215:134-138(1988).
-!- FUNCTION: IN NITROGEN-LIMITING CONDITIONS, WHEN THE
                                                                                       family
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Holtel A., Merrick M.;
"Identification of the Klebsiella pneumoniae glnB
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30;
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to the P(II) protein
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Nitrogen regulatory protein P-II.
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 602, 601, 623;
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MEDLINE=89201233; PubMed=2907369;
Holtel A., Merrick M.;
Holtel A., Merrick M.;
"Identification of the Klebsiella pneumoniae glnB gene: nucleot
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"Cascade control of Escherichia coli glutamine synthetase.
Purification and properties of PII protein and nucleotide seque
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E->Y: GLUTAMINE AUXOTROPHY
CC15D58A2F225507 CRC64;
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Pred. No. 4.4e-19;
5; Mismatches 28;
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PIR; S04377; S04377.
HSSP; P05826; 2PII.
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII glnB.UMP_S.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation.
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OR B2553 OR C3076 OR Z3829 OR ECS3419 OR
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(Rel. 21, Last sequence update)
(Rel. 42, Last annotation update)
                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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Mol. Gen. Genet. 215:134-138(1988)
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SPECIES=E.coli;
MEDLINE=87250488; PubMed=2885322;
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Salmonella typhi, and
Shigella flexneri.
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SEQUENCE FROM N.A.

SPECIES=E.coli; STRAIN=Ki2;

X MEDLINE=97349980; PubMed=9205837;

X Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,

A Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,

A Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

A Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

A Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Mada C.,

Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Mada C.,

Yamagata S., Horiuchi T.;

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- Kl2 genome corresponding to 50.0-68.8 min on the linkage map and

analysis of its sequence features.";

DNA Res. 4:91-113(1997).
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MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
*Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
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SPECIES=B.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
MEDLINB=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch | Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Slasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Shayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner R.R.;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
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Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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X-12.";
                                                                                                                                                       "Isolation and nucleotide sequence of the hmp
haemoglobin-like protein in Escherichia coli Mol. Gen. Genet. 226:49-58(1991).
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nB region of the Escherichia
eriol. 175:7441-7449(1993).
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MEDLINE=97426617; PubMed=9278503;
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=91238719; PubMed=2034230;
Vasudevan S.G., Armarego W.L.F.,
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MEDLINE=94042920; PubMed=8226691;
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                                                                                                                                          SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
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SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90089474; PubMed=2574599;
Magasanik B.;
"Regulation of transcription of the glnALG operon of Escherichia
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                                                       van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.; "The genes of the glutamine synthetase adenylylation cascade regulated by nitrogen in Escherichia coli."; Mol. Microbiol. 9:443-458(1993).
                                                                                                                                                                                                                                                   of Salmonella enterica serovar
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriol. 185:2330-2337(2003)
                   SEQUENCE OF 1-12 FROM N.A.
SPECIES=E.coli; STRAIN=K12 / W3110
MEDLINE=94018640; PubMed=8412694;
                                                                                                                                                                                                                                                      "Complete genome sequence
                                                                                                                                                                                                                                                                                Nature 413:852-856(2001)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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C STRAIN=ATCC 11170 / S1;

A Zhang Y., Ludden P.W., Roberts G.P.;

L Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

L Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE COLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE BYENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARATE DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE BOLD OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE BNZYME COLLISTING THE BNZYME COLLISTING THE POLITIAN OF GLUTAMINE SYNTHETASE, SO ACTIVATION OF GLUTAMINE SYNTHETASE, SO ACTIVATION OF GLUTAMINE SYNTHETASE 
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Rhodospirillaceae, Rhodospirillum.
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Pred. No. 6.8e-19;
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                                                                                                                                             SPECIES=E.coli;
MEDLINE=94123764; PubMed=8293810;
Vasudevan S.G., Gedye C., Dixon N.E., Cheah I
Suffolk P.M., Jeffrey P.D., Ollis D.L.;
"Escherichia coli PII protein: purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal
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01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
Nitrogen regulatory protein P-II.
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2:981-990(1994).
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STRAIN=ATCC 11170 / S1;
MEDLINE=96254013; PubMed=8704966;
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Conservative 25
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FEBS Lett. 337:255-258(1994)
protein phosphorylation."
ochimie 71:1005-1012(1989)
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MEDLINE=21396507; PubMed=11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Gloux Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; Ranalysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021. ";

Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arcondeguy I., Huez I., Fourment J., Kahn D.; "Symbiotic nitrogen fixation does not require adenylylation of glutamine synthetase I in Rhizobium meliloti."; FEMS Microbiol. Lett. 145:33-40(1996).
    and for
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                                                                                                                                                                                                                                                                                                                                                        Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nitrogen regulatory protein P-II.
GLNB OR R01639 OR SMC00947.
Rhizobium meliloti (Sinorhizobium meliloti).
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     land this statement is not remos requires a license agreement (an email to license@isb-sib.ch)
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GlnB_UMP_
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MEDLINE=97085050; PubMed=8931324;
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                                                     EMBL; X84158; CAA58963.1; -
EMBL; AF029703; AAB84167.1; PIR; S52328; S52328. HSSP; P05826; 2PII.
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                                                                                                 HSSP; POSBZ6; ZF11.
InterPro; IPR002187; PII_
InterPro; IPR002332; PII_
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Zinchenko V.V., Churin Y., Shestopalov V.I., Shestakov S.V.;

Zinchenko V.V., Churin Y., Shestopalov V.I., Shestakov S.V.;

"Nucleotide sequence and characterization of the Rhodobacter
sphaeroides glnB and glnA genes.";

Microbiology 140:2143-2151(1994).

-!- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE
GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED
GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALYZED
CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL
ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE
DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE
DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE
DEADENYLYLATION OF GLUTAMINE SYNTHETASE, SO ACTIVATING THE ENZYME.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See Line) or send an email in the statement is not removed.
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IS URIDYLYLATED TO P-II-UMP, THESE EVENTS ARE RESUBUNIT: Homotrimer (By similarity).
SIMILARITY: Belongs to the P(II) protein family.
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(Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                         EMBL; ALS91/01; CALSBERGE, 2PII.
HSSP; P05826; 2PII.
InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII GlnB UMP_S.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fi
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illarity 48.6%;
Conservative 27
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                                                                                                                                                                                                                                                                                                   EMBL; ALS91787; CAC46218.1;
                                                                                                                                                                                                                                                                             US0385; AAC44623.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homotrimer
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                                                                                            This SWISS-PROT
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01-NOV-1995
15-DEC-1998
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Best Local
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P43519;
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collaboration

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SUBUNIT: Homotrimer (By similarity).
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STRAIN=Rd / KW20 / ATCC 51907;

K MEDLINE=95350630; PubMed=7542800;

R Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

A Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

A Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

R Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

A Venter J.C.;

Webter J.C.;
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Science 269:496-512(1995).
Science 269:496-512(1995).
-;- FUNCTION: P-II INDIRECTLY CONTROLS THE TRANSCRIPTION OF THE GLUTAMINE SYNTHETASE GENE (GLNA). P-II PREVENTS NR-II CATALY:
CONVERSION OF NR-I TO NR-I-PHOSPHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II IS URIDYLYLATED TO P-II-UMP, THE EVENTS ARE REVERSED. WHEN THE RATIO OF GLN TO 2-KETOGLUTARAT DECREASES, P-II IS URIDYLYLATED TO P-II-UMP, WHICH CAUSES THE DECREASES, P-II IS URIDYLYLATED SYNTHETASE BY GLNE, SO ACTIVATI
   in
                                                                                                                                                                                                                                                                  3 KVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus infl
   non-profit institutions as long as the cand for cand this statement is not removed. Usage by and for crequires a license agreement (See http://www.isb-sib.ch/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                       112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Homotrimer (By similarity).
PTM: Uridylylated/deuridylylated by glnD (By similarity)
SIMILARITY: Belongs to the P(II) protein family.
                                                                                                                                                                                                                                                                                                                            63 EIVVSKDOVEDVIEKIIEBARTGEIGDGKIFLLPVSDVIRVRTGERGDKA
                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                             30,
                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                    UMP (BY SIMILARITY)
B278486AC9EB17D3
                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                        48.4%; Score 269.5; DB 46.4%; Pred. No. 2e-18;
                                                                                                                            PRINTS; PROC340; PIIGLNB.
PRINTS; PROC340; PIIGLNB.
PRODOM; PDC01194; PII GLNB UMP; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation.
                                                                                                                                                                                                                                                                                                                                                                                                 112 AA
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Mismatches
                                                                       PIR; S33180; S33180.
HSSP; P38504; 1GNK.
InterPro; IPR002187; PII_glnB.
InterPro; IPR002332; PII_GlnB_UMP_S.
Pfam; PF00543; P-II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nitrogen regulatory protein P-II GLNB OR HI0337.
                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                  12100 MW;
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                                                             CAA50650.1;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               influenzae.
                                                                                                                                                                                                   112 AA;
                                                                                                                                                                                                                                      Similarity
                                         send an email
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                                                              X71659;
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01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haemophilus
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       use by modified entities
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STRAIN=MAFF303099;

MEDLINE=21082930; PubMed=11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Matanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

RT Feuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium

RT Pesorhizobium loti.";

Nesorhizobium loti.";

DNA Res. 7:331-338(2000).

-!- FUNCTICN: IN NITROGEN-LIMITING CONDITIONS, WHEN THE RATIO OF GLN

CC TO 2-KETOGLUTARATE DECREASES, P-II IS URIDYLYLATED TO P-II-UMP. P-

TO 2-KETOGLUTARATE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS),

II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS),

II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASE (GS),

II-UMP ALLOWS THE DEADENYLYLATION OF GLUTAMINE SYNTHETASES P-II
                                                                                                                                                                     t is in no way and for commercial
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A). P-II PREVENTS NR-II CATALYZED CONVERSION OF NR-I TO
PHATE, THE TRANSCRIPTIONAL ACTIVATOR OF GLNA. WHEN P-II
(LATED TO P-II-UMP, THESE EVENTS ARE REVERSED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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49.1%; Pred. No. 2.5e-18;
ive 24; Mismatches 31;
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16-OCT-2001 (Rel. 40, Last annotation
Nitrogen regulatory protein P-II.
GLNB OR MLL0345.
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InterPro; IPR002332; PII glnB.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB UMP; 1.
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PII_GlnB_UMP_
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12640 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F64062.
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32718; AAC21
PIR; F64062; F64062
HSSP; P05826; 2PII.
TIGR; HI0337; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AA;
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SEQUENCE FROM N.A
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098NI8;
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002187; PII glnB.
InterPro; IPR002332; PII glnB.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
Transcription regulation; Nitrogen fixation; Complete proteome.
BINDING 51 51 UMP (BY SIMILARITY).
SEQUENCE 112 AA; 12200 MW; CF0F60FE7185465A CRC64;
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SIMILARITY: Belongs to the P(II) protein family.
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Search completed: May 24, 2004, 19:13:35 Job time : 11,5 secs

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		10,	10,	24,		communis (Castor bean).	e; Stre	phyta;	s; Eupl					8; PubMed=9811909;	an de	Arabid		U.S.A.	2.1; -		ne regu	ation	2187; PII_glnB.		В.	jlnB; 1	PII GINB CTER;		21781 MW;	100.0%;	100.0%; ive 0;
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72 FYKVEAILRPWRVSQVSSALLKIGIRGVTVSDVRGFGAQGGSTERQGGSEFSEDKFVAKV
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PII protein (P II nitrogen sensing protein GLB I) (At4g01900).
T7B11.16 OR AT4G01900.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Huang E.N., Nascimento L., de la Bastide M., Habermann K., Vil M
Preston R.R., Spiegel L.A., See L.H., Shah R., Matero A.,
O'Shaughnessy A., Rodriguez M., Shekher M., Swaby I., Schutz K.,
Parnell L.D., Dedhia N.N., McCombie W.R.;
"Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Spiegel L.A., Huang B.N., Nascimento L.U., de la Bastide M., Vil
Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.
Preston R.R., Matero A., See L.H., Swaby I., Habermann K., Dedhia
Shekher M., Schutz K., Mayer K.F.X.;
Mewes H.W., Lemcke K., Mayer K.F.X.;
Anhmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lan Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C. Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                            SEÇUENCE FROM N.A.
MEDLINE=99030678; PubMed=9811909;
Hsieh M.H., Lam H.M., van de Loo F.J., Coruzzi G.;
"A PII-like protein in Arabidopsis: putative role in nitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9, P05826; 2PII.
GO:0030234; F:enzyme regulator activity; IEA.
GO:0006808; P:regulation of nitrogen utilization; IEA.
erPro; IPR002187; PII_glnB.
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EMBL; AC007138; AAD22652.1;
EMBL; AL161493; CAB80683.1;
EMBL; BT005209; AAO63273.1;
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Proc. Natl. Acad.
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HSSP; P38504; 1GNK.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization;
InterPro; IPR002187; PII_glnB.
Pfam; PF00543; P-II; 1.
PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII_glnB; 1.
ProDom; PD001194; PII_GLNB_CTER; 1.
PROSITE; PS00638; PII_GLNB_CTER; 1.
                                                                                                                                                                                                                                                                                                                                                           Medicago sativa (Alfalfa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifol
NCBI_TaxID=3879;
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NCBI_TaxID=103690;
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8.9e-41; 7;
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85.8%; Pred. No. 3.7e-39;
ive 8; Mismatches 8;
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"Characterization of PII (GLNB) in alfalfa.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
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01-OCT-2000 (TrEMBLrel. 15, L
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90.3%;
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97; Conserv
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SEQUENCE FROM N.A.
STRAIN-PCC 7120;
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                      Query Match
Best Local Similarity
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C3F0AA5625E9F870 CRC64;

12432 MW;

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Similarity
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                                                            Similarity
  112 AA;
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QBDLAS;
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"Phosphorylation of the signal transduction protein PII by the kinase PknC in the cyanobacterium Anabaena sp. strain PCC 7120. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.
Watanabe A., Iriguchi M., Matsumoto M., Matsuno A., Muraki A.,
Kishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
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EIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRIRIGEKNTEA
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EMBL; AF120107; AAF63031.1; -.

HSSP; P05826; 2PII.

G0; G0:0030234; F:enzyme regulator activity; IEA.

G0; G0:0006808; P:regulation of nitrogen utilization; IEA.

InterPro; IPR002187; PII glnB.

InterPro; IPR002332; PII GlnB UMP S.

Pfam; PF00543; P-II; 1.

PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00496; PII GLNB UMP; 1.
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PIR; AH2095; AH2095.
HSSP; P05826; 2PII.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII_GlnB_UMP_S.
InterPro; IPR002332; PII_GlnB_UMP_S.
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus
NCBI_TaxID=32049;
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on update)
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Pred. No. 1.4e-22;
2; Mismatches 23;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Nitrogen metabolism regulator protein.
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ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
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DNA Res. 8:205-213(2001).
EMBL; AJ251822; CAB75358.1; -.
EMBL; AP003589; BAB74018.1; -.
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.larity 58.2%;
Conservative 22
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STRAIN=PCC7002;
Sakamoto T., Gruber T., B
"Nucleotide sequence of g
PCC7002.";
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EMBL; AP005370; BAC08143.1; -.

GO; GO:0030234; F:enzyme regulator activity; IEA.

GO; GO:0006808; F:regulation of nitrogen utilization; IEA InterPro; IPR002187; PII glnB.

InterPro; IPR002332; PII glnB.UMP.S.

Pfam; PF00543; P-II; 1.
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           Length
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Last annotation update)
P-II 1.
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Nitrogen regulatory protein P-II.
Symperhome
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larity 58.2%; Pred. No. 3.5e-22;
Conservative 21; Mismatches 24;
56.3%; Score 313.5; DB 2; 56.6%; Pred. No. 2.2e-22;
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ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
                                                  24;
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01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-OCT-2003 (TrEMBLrel. 25, L
Nitrogen regulatory protein P
GLNB OR NMA0447.
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Bacteria; Cyanobacteria;
NCBI_TaxID=32046;
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                                                     Conservative
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AE002548; AAF42322.1
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Best Local Similarity
Matches 62; Conser
                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 112 AA;
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Matches 59
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Q8GQS4
ID Q8GOS
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                                                                                                                                      SECUENCE FACTOR W. S. SELOCKYPE 4A;

STRAIN=22491 / Serogroup A / Serockype 4A;

KEDLINE=20222556; PubMed=10761919;

REDLINE=20222556; PubMed=10761919;

KIEE S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

A Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

A Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Kajandream B.A., Spratt B.G., Barrell B.G.;

Whitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria

meningicidis Z2491.";

Nature 404:502-506(2000).

REMBL; AL162753; CAB83744.1; -.

REMBL; AL162753; CAB83744.1; -.
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STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelsor Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark Mason T., Ciecko A., Masignani V., Pizza M., Grandi G., Sun L., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                               Meisseriales
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GO:0030234; F:enzyme regulator activity, IEA.
GO:0006808; P:regulation of nitrogen utilization;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 303.5; DB Pred. No. 2e-21; 25; Mismatches 2
          Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria;
Neisseriaceae; Neisseria.
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Interpro; IPR002332; PII GlnB UMP_
Pfam; PF00543; P-II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00340; PIIGLNB.
Procom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER;
PROSITE; PS00496; PII GLNB UMP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.5%; Scilarity 54.5%; Pr
Conservative 25;
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60; Conser
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                                                                            TaxID=65699;
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                                                                                                                           PROM N
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01-OCT-2060
01-OCT-2003
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MEDLINE=22825698; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects of
niche differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 EIVVSKDQVEDVIBKIIBEARIGEIGDGKIFLLPVSDVIRVRIGERGDKA | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.11 | 1.
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PIR; B81019; B81019.

HSSP; P05826; 2PII.

TIGR; NMB1995; -.

G0; G0:0030234; F:enzyme regulator activity; IEA.

G0; G0:0006808; P:regulation of nitrogen utilization; IEZ.

InterPro; IPR002187; PII glnB.

InterPro; IPR002332; PII glnB.

PETAM; PF00543; P-II; 1.

PRODOM; PD001194; PII glnB; 1.

PROSITE; PS00638; PII GLNB CTER; 1.

PROSITE; PS00496; PII GLNB UMP; 1.
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es 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1arity 53.6%; Score 302.5; DB Conservative 26; Mismatches 2
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Last sequence up
Last annotation 1
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56.4%; Pred. No. 2.5(
ive 19; Mismatches
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EMBL; BX572099; CAE21656.1;
Complete proteome.
SRQUENCE 112 AA; 12362 M
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                                                                RESULT 12
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                                                                         Bacteria; Proteobacteria; Alphaproteobacter diazotrophicus).
Acetobacteraceae; Gluconacetobacter.
NCBI_TaxID=33996;
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MEDLINE=22825697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L
Lamerdin J., Regala W., Allen B.E., McCarren J., Paulsen
Dufresne A., Partensky F., Webb E.A., Materbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
EMBL; BX569690; CAE06977.1; -.
Complete proteome.
SEQUENCE 112 AA; 12340 MW; 387C54E0F85EEFD3 CRC64;
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NOV-2000) to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.2e-20;
5; Mismatches 26;
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Pred. No. 1.2e-20;
26; Mismatches 26;
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Bacteria; Cyanobacteria; Chroococcales;
NCBL_TaxID=84588;
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PRINTS; PR00340; PIIGENB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00496; PII GLNB UMP; 1.
SEQUENCE 112 AA; 12431 MW; 52AB
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Regulatory protein PII.
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Submitted (NOV-2000)
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01-GCT-2003
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STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486;
Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M. Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.; "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome."; Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).

EMBL; AR017165; AAQ00660.1; -.
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MEDLINE=22040572; PubMed=12045242;

Comanducci M., Bambini S., Brunelli B., Adu-Bobie J., Arico B.,

Capecchi B., Giuliani M.M., Masignani V., Santini L., Savino S.,

Granoff D.M., Caugant D.A., Pizza M., Rappuoli R., Mora M.;

"NadA, a novel vaccine candidate of Neisseria meningitidis.";

J. Exp. Med. 195:1445-1454(2002).

EMBL; AF452475; AAM53097.1; -.

GO; GO:0030234; F:enzyme regulator activity; IEA.

GO; GO:0006808; P:regulation of nitrogen utilization; IEA.

InterPro; IPR002332; PII_GINB.

R Pfam; PF00543; P-II; 1.
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein P-II (Fragment).
Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Length
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Nitrogen regulatory protein PII.
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llarity 52.7%; Pred. No. 2.3e-20;
Conservative 24; Mismatches 27;
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                                                                        Length 108;
                                                                                                                                                                                                                                                                                                    Azoarcus sp. BH72.
Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
Rhodocyclaceae; Azoarcus.
NCBI_TaxID=62928;
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MEDLINE=20521930; PubMed=11069654;
MEDLINE=20521930; PubMed=11069654;
Martin D.E., Hurek T., Reinhold-Hurek B.;
Martin D.E., Huree PII-like signal transmitter proteins
diazotrophic proteobacterium Azoarcus sp. BH72.";
Mol. Microbiol. 38:276-288(2000).
EMBL; AF281017; AAG40188.1; -.
HSSP; P05826; 2PII.
GO; GO:0030234; F:enzyme regulator activity; IEA.
GO; GO:0006808; P:regulation of nitrogen utilization; IE/
InterPro; IPR002187; PII glnB.
InterPro; IPR00232; PII glnB.
InterPro; IPR002332; PII glnB. 1.
ProDom; PD001194; PII glnB. 1.
ProDom; PD001194; PII glnB. 1.
PROSITE; PS00638; PII GLNB CTER; 1.
PROSITE; PS00638; PII GLNB UMP; 1.
RROSITE; PS00696; PII GLNB UMP; 1.
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                                                     CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
P2-like signal transmitter protein GlnB.
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Pred. No. 6.5e-20;
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   PRINTS; PR00340; PIIGLNB.
ProDom; PD001194; PII glnB; 1.
PROSITE; PS00638; PII GLNB CTER;
PROSITE; PS00496; PII GLNB UMP;
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STRAIN=strain PCC 9511;
A Falinska K.A., Loiseaux-de Goer S., Blondel A., ...
A Rippka R., Tandeau de Marsac N.;
A Rippka R., Tandeau de Marsac N.;
Tin spite of synthesizing a cyanobacterial-type PII protein, the coeanic photosynthetic prokaryote Prochlorococcus marinus, strain spite of synthesizing a cyanobacterial-type PII protein, the STRAIN SUBJECT OF BENEL, From No. 1000 Coeanic photosynthetic prokaryote Prochlorococcus marinus, strain strain is unable to utilize nitrate. ";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
BENEL, AJ271089; CAB87556.1; -..
DR HSSP; P38504; IGNK.
GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
DR GO; GO:0006808; P:regulation of nitrogen utilization; IEA.
InterPro; IPR002187; PII glnB.
InterPro; PII; 1...
Prochlorococcus sp. (strain PCC 9511).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
NCBI_TaxID=100363;
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Pred. No. 8.5e-20;
5; Mismatches 28;
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InterPro; IPRUUZAC.

Pfam; PF00543; P-II; 1.

PRINTS; PR00340; PIIGLNB.

ProDom; PD001194; PII glnB; 1.

PROSITE; PS00638; PII GLNB CTER; 1

PROSITE; PS00638; PII GLNB CTER; 1

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8         285.8         34.9         8 AC007138         AR027892         AR027892           9         246         30.1         120185         8 AC007138         AC007138         AC007138           11         246         30.1         120185         8 AC007138         AC007138         AC007138           12         246         30.1         120185         8 PP14499604         AC007138         AC007138           13         20.6         25.7         1085         8 PP14499604         AC007138         AC007136           14         39.4         24.4         90.2         8 AK06407         AC007136         AC007136           16         109.8         13.1         164921         B AK09152         AC007136         AC007136           10         13.4         30.4         1 PDGLMBPRT         AC007136         AC007136         AC007136           10         13.1         164921         1 AC017165         AC007136         AC007136         AC007136           10         13.1         164921         1 AC01714         AC007136         AC007136         AC007136           10         13.0         14.4         90.2         8 AC007143         AC007147         AC007147	8         285         34.9         84.0         8         AK095454         AR095454           9         253.8         31.1         796         8         AY077892         AY077892           10         246         30.1         120185         8         AC007138         AY442185           11         246         30.1         120186         8         AC007138         AV442185           12         245         30.0         9         AY608407         AK089152         AK442185           13         20.4         90.2         8         AK089152         AK068407         AK0891604           199.4         24.4         90.2         8         AK099152         AK0891604         AK0991604           10         13.1         30.2         8         AK099162         AK099162         AK099162           10         13.1         30.2         8         AK099162         AK0991604         AK0991604           10         13.1         30.2         8         AK099162         AK099162         AK0991604           10         13.1         30.2         8         AK099162         AK099162         AK099162           10.0         13.1         30.2 <td>8         285         34.9         84 0         8 AF095454         AF095454         AF095454           9         253.8         31.1         796         8 AY077892         AY077892         AY077892           11         246         30.1         120185         8 AY077892         AY442185         AY442185           13         246         30.1         120186         8 PP1489604         AY442185         AY442185           13         209.6         25.7         1085         8 PP1489604         AY442185         AY442185           15         19.4         24.4         902         8 AY099152         AY069152         AY069152           16         109.8         13.4         24.4         902         8 AY099152         AY069152         AY069152           16         109.8         13.4         24.4         902         8 AY099152         AY0691727         AY0691727           17         107.4         21.4         91.8         1 AY099152         AY069177         AY07917           20         13.0         24.9         1 AY079137         AY079137         AY079137         AY079137           21         10.6         13.0         24.9         1 AY079137         AY079137</td> <td>7</td> <td>m</td> <td>_:</td> <td>Ŋ</td> <td>Ġ</td> <td>255</td> <td>25592 Sequence</td>	8         285         34.9         84 0         8 AF095454         AF095454         AF095454           9         253.8         31.1         796         8 AY077892         AY077892         AY077892           11         246         30.1         120185         8 AY077892         AY442185         AY442185           13         246         30.1         120186         8 PP1489604         AY442185         AY442185           13         209.6         25.7         1085         8 PP1489604         AY442185         AY442185           15         19.4         24.4         902         8 AY099152         AY069152         AY069152           16         109.8         13.4         24.4         902         8 AY099152         AY069152         AY069152           16         109.8         13.4         24.4         902         8 AY099152         AY0691727         AY0691727           17         107.4         21.4         91.8         1 AY099152         AY069177         AY07917           20         13.0         24.9         1 AY079137         AY079137         AY079137         AY079137           21         10.6         13.0         24.9         1 AY079137         AY079137	7	m	_:	Ŋ	Ġ	255	25592 Sequence
9         253.8         31.1         796         8         AY022892         AY027892           10         246         30.1         198220         8         AYCHENYS         AY442185         AY4442185         AY4442185         AY4442185         AY4442185         AY4442185         AY4442185         AY4442185         AY66407         AY66607         AY66607         AY66607	9         253.8         31.1         796         B AY027892         AY027892           10         246         30.1         120185         B AYCRIN38         AY442185           11         245         30.1         198220         B AYCRIN4S         AY442185           12         245         30.0         1987         B PP1489604         AX068407           13         203.6         25.7         1085         B PP1489604         AX068407           14         199.4         24.4         902         B AX069152         AX069152           15         199.4         24.4         902         B AX0699152         AX0699152           10         13.9         13.1         16493         1         AX0699152           10         13.0         2493         1         AX079176         AX079152           20         13.0         2443         1         AX079153         AX0772186           21         10.6         13.0         2493         1         AX0772186           21         10.6         13.1         14803         1         AX0772186           22         10.6         13.0         14803         1         AX077709	9         253.8         31.1         796         B AY027892         AY027892           10         246         30.1         120185         B AY027185         AY442185           11         245         30.1         198220         B AYCHERIVS         AY440964           13         245         30.0         947         B PP14489604         AY066407           14         199.4         24.4         902         B AY069152         AY066407           15         199.4         24.4         902         B AY069152         AY069152           16         109.6         13.1         16493         1         AX069152           18         106.8         13.1         16493         1         AX069152           18         106.8         13.1         16493         1         AX069164         AX069164           18         106.8         13.1         16493         1         AX01165         AX07127         X97272           19         13.0         14180         1         AX01166         AX071166         AX071166         AX071166         AX071166           21         10.2         14.4         1910.2         B AX071169         AX071166         AX071166 <td>œ</td> <td><math>\alpha</math></td> <td></td> <td>84</td> <td>œ</td> <td>9545</td> <td>95454 R</td>	œ	$\alpha$		84	œ	9545	95454 R
10	10         246         30.1 120185         8 ACGO07138         ACGO071	10   246   30.1   120185   B ACGONTIS   AC	თ	53.	•	7	œ	789	27892
11   246   30.1   19820   8 ATCKRIV5   ALIGHRES   ALI	11         246         30.1         198220         8         ATCHRIVS         ALJ64185           12         245         30.0         947         8         PP14495604         AX4096185           13         209.4         25.7         1085         8         PP14495604         AX4099152           14         199.4         24.4         902         8         AX608407         AX609152           15         109.8         13.4         364         1         FDGLMBPRT         AX609152           16         13.0         13.4         36.2         1         AX609152         AX609152           10         13.1         16423         1         AX6017165         AX609152         AX609152           10         13.0         341880         1         AX6017165         AX6017165         AX6017165           20         10.6         13.0         341880         1         AX6017165         AX6017165           21         10.2         13.0         1480         1         AX6017165         AX6017165           21         10.2         13.1         AX6017165         AX6017165         AX6017167           22         10.2         13.4         AX60171	11   246   30.1   198220   8   ATCHRIVS   ALIACIAGS	10	24	~	1201	œ	713	07138
12         245         30.0         947         B         AV442185         AV442185         AV442185           13         20.6         25.7         1005         8         PP1480604         AX069407         AX069152           14         199.4         24.4         90.2         8         AX069407         AX069152         AX069152           16         199.4         24.4         90.2         8         AX069152         XX099152         XX099152           10         13.4         3.4         1         PD6LNBRT         AX091152         XX099152         XX091175         XX091176	12         245         30.0         947         B AY442185         AY442185         AY442185           13         203.6         25.7         1085         8 PP1489604         AX068407         AX0689152           14         202.6         8 AX068407         AX0699152         AX0699152         AX0699152           15         134         324         902         8 AX058128         AX069152         AX069152           10         13.4         334         1 F0GMBRRT         X809152         X8099152           10         13.4         330143         1 AR01165         AX059152         AX059152           20         16         13.0         24438         1 AR01286         AR012186         AX051862           21         10.2         12.5         262202         1 AR013894         AX051862         AX051862           22         10.6         13.0         3498         1 AR013894         AX051862         AX051862           24         98         12.0         686         1 AR013894         AX051862         AX051862           25         11.7         343         1 SX013894         AX051862         AX051862           26         11.7         343         1 SX013894 </td <td>  13</td> <td>11</td> <td>T</td> <td>~</td> <td>19822</td> <td>œ</td> <td>RIV</td> <td>61493</td>	13	11	T	~	19822	œ	RIV	61493
13   200.6   25.7   1085   8   PPI489604   AA489604     14   199.4   24.4   90.2   8   AK008407   AK068407     15   109.4   24.4   90.2   8   AK099152     16   109.8   13.4   30.143   1   AK011165   AK071165     18   106.8   13.1   164921   1   AK011165   AK071165     100.8   13.1   164921   1   AK011165   AK071165     100.8   13.1   164921   1   AK011165   AK071165     100.1   13.0   341880   1   AK001389   AK071389     100.2   12.5   26220   1   AK079137   AK079137     23   98.6   12.1   4348   1   AK079137   AK079137     24   98   12.0   686   1   AK079137   AK079137     25   95.8   11.7   339   1   AK070674   AK0005074     26   95.8   11.7   339   1   AK070674   AK0005074     26   95.8   11.7   32935   1   AK006746   AK006766     24   91.6   11.5   349746   1   AK0706768   AK006766     25   92.8   11.4   96109   6   AK08756   AK006766   AK006766     26   92.8   11.4   96109   6   AK08756   AK006766   AK006767     27   93.2   11.5   349740   1   AK006746   AK006766     28   94.2   11.5   349740   1   AK006746   AK006766     29   94.2   11.5   349740   1   AK006746   AK006766     20   94.2   11.5   349740   1   AK006746   AK006766     20   94.2   11.5   AK006746   AK006746   AK006746     20   94.2   11.4   96109   6   AK006740   AK006746   AK006746     20   94.8   10.9   35.1   AK00680   AK00680   AK00680     20   94.8   10.9   35.1   AK00680   AK00680   AK00680     20   94.8   10.9   36.2   AK00680   AK00680   AK00680     20   94.8   10.9   36.2   AK00680   AK00680   AK00680     20   94.8   10.9   36.2   AK00680   AK00680   AK00680     20   94.8   10.9   AK00680   AK00680   AK00680     20   94.8   10.9   AK00680   AK00680   AK00680   AK00680     20   94.8   10.9   AK00680	13         209.6         25.7         1085         8         PPI489604         AA489604           14         195.4         24.4         902         8         AK009122         AK009125           15         195.4         24.4         902         8         AK009122         AK099122           16         109.8         13.4         384         1         PDGLNBPRT         AK072186           10         10.6         13.1         164913         1         AK001165         AK072186           20         10.6         13.1         164913         1         AK001165         AK072186         AK072186         AK072186           21         10.6         13.0         341880         1         AK072186	13   209.6   25.7   1085   8   PF1489604   AJ489604     14   199.4   24.4   90.2   8   AK068407   AK068407     15   109.4   13.1   300143   1   AK068407   AK068407     16   109.8   13.4   90.2   8   AK068407   AK068407     10   10.4   13.1   300143   1   AR011165   AR011165     10   10.6   13.0   2493   1   AR011165   AR011165     10   10.6   13.0   2493   1   AR011165   AR011165     10   13.0   341880   AR0118980   AR0118980     10   12.1   24921   8   AF07137   AF071389     10   12.1   2493   1   AF07137   AF071319     10   12.1   4348   1   AF07137   AF0719137     11   13   13   1   AR01169   AR01189   AR0118980     12   10.2   383   1   AR01149   AR011991     13   11   13   1   AR01149   AR01149   AR011499     14   11.5   30205   1   AR01189   AR011890   AR0016508     15   10.9   34   1   AR01189   AR01189   AR011890     11   24795   1   AR01189   AR01189   AR011890     12   30   31   AR01189   AR01189   AR011890     13   30   31   AR01189   AR01189   AR011890     14   11.5   30205   1   AR01189   AR011890   AR011890     15   30   30   30   AR01189   AR011890   AR011890     16   3   3   3   4   AR01189   AR011890   AR011890     18   4   10   3   3   3   4   AR01189   AR01189   AR011890     14   88.4   10.9   3   3   4   AR01189   AR011890   AR011890     15   30   30   30   30   AR011890   AR01	11	i <del>d</del> i		94	Œ	4218	42185 Lycope
14   199.4   24.4   902   8   AKO68407   AKO68407   AKO68407   24.4   902   8   AKO699152   AKO99152   109.8   13.4   13.4   902   8   AKO69152   AKO99152   AKO99152   100.8   13.4   13.4   902   8   AKO99152   AKO99152   AKO99152   AKO99152   100.8   13.1   164921   8   AKO2186   AKO72186   AKO72188   AK	Machine   Mach	4   199.4   24.4   902   8   AKO68407   AKO68407   AKO68407   24.4   902   8   AKO68407   AKO69152   AKO99152   AKO99152   109.4   24.4   902   8   AKO69152   AKO99152   AKO99152   AKO99152   20   20   20   20   20   20   20	: er	60		10	00	4896	89604 Pinus
15   199.4   24.4   90.2   3   AKO99152   AKO99158	199.4   24.4   902   8   AKO99152   AKO99152   15   159.4   24.4   902   8   AKO99152   AKO99152   15   100.8   13.4   304141   AB017165   AB017169   AB017169   AB017169   AB0171761   AB017171   AB017771   AB01777   AB017771   AB017771   AB017771   AB017771   AB017771   AB01777   AB017771   AB01777   AB017771   AB01	15	) * † F	, 0	` _		α	S RAO	68407 Orvza
15   199.4   24.4   20.2   ANOTATION   A	15   199.8   14.4   302   4   4   4   4   5   5   5   5   5   5	15	<b>#</b> L	, n c		7 6	0 0		99152
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18   106.   13.0   1492182   14921822   120   120   13.0   141880   1   140921822   120   13.0   141880   1   140921822   120   12.5   262202   1   12.5   262202   2622	18         106.8         13.1 164921         6 AF022188         AF022188         AF013589         AF0150589         AF01369	18   106.8   13.1   145921   8   AF8251812   AA58251812			ς.	1000	<b>-</b> 1 (	0 T C E	ALTER CAPACIO
19   106   13.0   2493   1 ASP218122   AP0013689 Nostcool     102   106   13.0   13.	106   13.0   2493   1 ASPZ51822   APDG5892 Macroscope   12.5 262202   1 BE572094   E8572094 Prochlo   102   10.5   13.0   341880   1 APDG5893   E8572094 Prochlo   10.5   12.5 262202   E8572094   E8572094 Prochlo   10.5   12.5 262202   E8572094   E8572094 Prochlo   10.5   12.5   1	19 106 13.0 2493 1 ASP21822 AD013589 Nostcool 21 102 13.0 349804 BY21822 AD013589 Nostcool 22 101.6 12.4 191028 B PPU38804 AP079137 AP0791	H	06.	~	16492	<b>3</b> 0	D (C	000177
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21     102     12.5     562202     1     BK5722994     U38604     PPUJB804       22     101.6     12.4     191028     8     PPUJB804     PPUJB804     PPUJB804       24     98     12.0     686     1     AF079137     AF079137     Synechoc       25     97     11.9     383     1     SYGGINB     AF077419     M62447     Synechoc       26     95.8     11.7     339     1     PMA271089     AE000674     AG006674     AG01689     Prochloc       26     95.2     11.7     30230     1     AP005691     AE000674     Aguifex       29     94.2     11.7     30230     1     AP005370     AP005310     AP005310     AP005370     Thermos       31     94.2     11.5     302050     1     AP006568     AP005340     AP005370     Thermos       32     94.2     11.5     300045     1     AR006568     AR006568     Gloeba       31     92.8     11.4     96109     6     AX067460     AX067460     Sequenc       32     91.6     11.2     247950     1     AR016802     AR016802     AX067460     AX067460     AX067460       34     89.4     <	21     102     12.5     26202     1     BK5772094     BK572094     138004     Poculto U38804     Poc	21 102 12.5 262202 1 RF572094 U38804 Porphyza 23 98.6 12.1 4448 1 AF079137 AF079137 Synecho 24 98.6 12.1 4448 1 AF079137 AF079137 Synecho 25 95.6 12.1 438 1 AF079137 AF079137 Synecho 26 95.8 11.7 3123 1 SYOGLNB ACTORN A	C)	<b>(2)</b>	~	34188		<b>TO</b> (	UJJOY NOBLOC
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DEFINITION	Sequence 13 from patent US 61//2/3	US 61//2/5.	
ACCESSION	AR125589		
VERSION	AR125589.1 GI:14111651		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 817)		
AUTHORS	Coruzzi, G.M., Lam, HM. and Hsieh, MH.	and Hsieh, MH.	
TITLE	Plant nitrogen regulatory P-PII genes	ry P-PII genes	
JOURNAL	Patent: US 6177275-A 13 23-JAN-2001;	23-JAN-2001;	
FEATURES	Location/Qualifiers	fiers	

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                    Score 817; DB 6; I
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Mismatches 0;
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Arabidopsis thaliana (thale cress)
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Spermatophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 844)
Hsieh,M.H., Lam,H.M., van de Loo, F.J. and Coruzzi,G.
A PII-like protein in Arabidopsis: putative role in nitrogen
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Hsieh, M.H., Lam, H.M., van de Loo, E
Direct Submission
Submitted (29-SEP-1998) Biology, Mashington Square East, New York,
Location/Qualifiers
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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241 GTCAGACCATGGAGATTCCATCGGCTTTACTGAAATCGGGATTCGAGGT 300 333 GTTACTGTTTCTGATGAGGGTTTGGTGCAAGGAGGTTCTACCGAGAGACACGGT 392 301 GTTACTGTTTCTGATGTGAGAGGGTTTGGTGCAAGGAGGTTCTACCGAGAGACACGGT 360 393 GGCTCTGAGTTCTCGAAGACAATTTGTTGCTAAAGTTAAGATCTACCGAGAGACACGGT 360 393 GGCTCTGAGTTCTCGAAGACAAATTTGTTGCTAAAGTTAAGATCGAAGGACACGGT 420 453 AAAGACCAAGTTCTCGAAGATTTGTTGCTAAAGTTAAGATCGAAGGACAGGAAGATT 512 421 AAAGACCAAGATTTTTGTTTTGTTTGTTGAAGGACAAGGACAGGAGAGATT 480 513 GGTGATGGCAAGATTTTTGTTTTGCCTGTCACAAGATCATAAGAAGACAAGGACAGGAGAAGATT 480 513 GGTGATGGCAAGATTTTTGTTTTGCCTGTCACAGATCATAAGAAGACAAGGACAGGAGAAGATT 480 513 GGTGATGGCAAGATTTTTGTTTTGCCTGTCACAGATCATAAGAAGACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA		WAL
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                     Kim,C.J. (SSP/Salk) and Seki,M. (
this work. Shinozaki,K. (RIKEN G
contributed equally to this work
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Pred. No. 2.1e-129;
Dr Mismatches 0;
                                                 Unclassified.

Unclassified.

(bases 1 to 588)

Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.

Plant nitrogen regulatory P-PII genes

Patent: US 6177275-A 15 23-JAM-2001;

Location/Qualifiers
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Ricinus communis (castor bean)
Ricinus communis
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Acalypheae; Ricinus.
1 (bases 1 to 840)
Hsieh,M.H., Lam,H.M., van de Loo,F.J. and Coruzzi,G.
A PII-like protein in Arabidopsis: putative role in nitrogen
sensing
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M. Direct Submission
Submitted (29-SEP-1998) Biology, New York University, 100 Washington Square East, New York, NY 10003, USA Location/Qualifiers
                 Score 285; DB 6; 1
Pred. No. 2.8e-57;
1; Mismatches 165;
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Ricinus communis PII protein mRNA,
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                   ch 34.9%;
1 Similarity 70.3%;
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Pred. No. 1.3e-57;
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   1 (bases 1 to 897)
Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-F
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 14 23-JAN-2001;
Location/Qualifiers
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US 6177275
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/organism="unknown"
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10 CM,
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/codon_start=1
/product="Pll protein"
/protein_id="AAK16221.1"
/protein_id="AAK16221.1"
/db_xref="Gl:13277515"
/translation="MTLIAKPNVFNGLNFNINETQIPFSSFSVIRKRFGDSSHRNVVLRSNGNASVLPKIRAQNLPDYVPESKFYKVEAILRPWRIPQVSSGLLKMGIRGVTVSDVRSNGNASVLPKIRAQNLPDYVPESKFYKVEAILRPWRIPQVSSGLLKMGIRGVTVSDVRGFGAGGSEFSEDNFVAKVKMEIVVRKDQVEAVINKIMETARTGEIGDGKIFLIPVSDVIRIRTGERGEQAERMAGGLTDALYV"
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Knox and College, Las Cruces, NM 88003,
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2 (bases 1 to 796)

Garcia-Ibilcieta, D. and Sengupta-Gopalan, C.
Direct Submission

Submitted (22-FEB-2001) Molecular Biology 1

University, Corner of Knox and College, Las
                                                  Sengupta-Gopalan, C. (GENB) in alfalfa
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'mol_type="mRNA"
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                                                                                                                                                                                                /translation="HBATAKLGLLTPLHSNNIKKEFPVFDFSLFCPELRHSRFSHFNT
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DVRGFGAQGGSTERQGGSEFSEDKFVAKVKMBIVVSKDQVEDVIEKIIEBARTGEIGD
GKIFLLPVSDVIRVRTGERGDKAERMTGGRSDMSTSA"
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/product="PII protein"
/protein_id="AAC78332.1"
/db_xref="GI:3885941"
                                                                                                  /function="putative rol
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                          /organism="Ricinus co
/mol_type="mRNA"
/db_xref="taxon:3988"
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/gene="T7B11.4"
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FillGvplpwpgsplilfpnkvsspsyasslsphaksewrnytiaoaakfvatvotavsspellgvplsphaksewrnytiaoaakfvatvotavsspellfprinklisvsrokhoekvlviaedyitlykvnekmpghavlippalds
Ktaysfgsogffnftarrpohiloilelgynvmyndvdmymlodppgylegshdayft
DDmpoikplnhshblpapdongetyicscmiylrptngaklimkkwseelosoawses
Irfkandopafnlalnktahovdlyllsovafptgglyfndamvketkgkhvivhnn
Yligydrkmrrfodyglwlvddhalesplgklo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724

Arabidopsis thaliana BAC T7B11 from chromosome IV near 9.5 cM

The T7 end of T7B11 is oriented toward the NOR and overlaps with T15B16, GenBank accession number AF104919. The SP6 end of T7B11 is oriented toward the centromere and overlaps with T10M13, GenBank accession number AF001308. There are no discrepancies found in these independently finished overlaps. The region from position 110064 to 110253 exists as single stranded and single chemistry. Incation/Qualifiers
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ad, Cold Spring
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                                                                                                                    eophyta;
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                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Wiridiplantae; Streptophyta; Eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 120185)
Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K.,
Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Materc
O'Shaughnessy, A., Rodriguez, M., Shekher, M., Swaby, I., Schutz, K.
Parnell, L.D., Dedhia, N.N. and McCombie, W.R.
Arabidopsis thaliana BAC T7B11 from chromosome IV near IO cM
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/gene="T7B11.2"
/note="encodes putative CHP-rich zinc finger prof
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Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K., Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K., Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., O'Shaughnessy, A., Rodriguez, M., Shekher, M., Swaby, I., Schi Parnell, L.D., Dedhia, N.N. and McCombie, M.R.

Direct Submission

Submitted (23-MAR-1999) Lita Annenberg Hazen Genome Sequer Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Conter, NY 11724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1561,1668.
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'mol type="genomic DNA"
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| oin{50. .556,1098. .1259,1340.
| gene="T7B11.1"
| note="identical to T15B16.9, G
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evidence=not_experimental
'product="hypothetical protein"
'protein_id="AAD22637.1"
'db_xref="GI:4558544"
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="IV"
                                                                        (thale cress)
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Parnell, L.D.
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VYSEVNIFGCSACHKIFNGFRYFHEDTKLDVLCGSFSEPFIHPSHPHPLYCISPEDD
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SEDLEQRQKEELHEKIIRLERQIDQVQAIELEVEQLKGQLNVMKHMASDGDAQVVKEV
DIIPKDLVEKEAELADLNKFNQTLILRERRTNDELQEARKELVNCMGELVRKPFVDAM
QQKYCQEDVEDRAVEVLQLWEHYINDPDWHPYKRVKLENQDREVEVIDDRDEKLRELK
ADLGDGPYNAVTKALLEINEYNPSGRYITTELWNFKEDKRATLEEGVTCLLDQWEKAK
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DQPAFNLALNKTAHQVDLYLLSQVAFPTGGLYFKNEAWVQETKGKHVIVHNNYIIGYD
RKMKRFQDYGLWLVDDHALESPLGKLE"
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LRDEYILRGLNNGLLFDKAYRVDGHGKKDWMKKDGPKLGLYGWIAGADDYNVDGREGE
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CDICEKETNPNTWFYTCKDHRASLHTWCVLGDFMGLIPKSTIELWNISYEVVLNNSIS
RPICRHCKSHCIPPIILKKIGTSDPYFCSLDCIESFKRLWRAK"
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AF104919; similar to A. thaliana CHP-rich proteins encode
by T10M13, GenBank accession number AF001308; functional
accession number AF104919
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functional catalog ID=99"
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number AF104919; gene
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T15B16.7, GenBank accession number AF1(
last edited on 3 Mar 99"
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                        GenBank
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"rote="identical to T15B16.7,
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oin(8080. .8568,9318. .9479,
gene="T7811.3"
/note="identical to T15B16.8
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complement(2647. .4650)
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/codon_start=1
/evidence=not_experim
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'note="identical to
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QVPRFLGLKVGLIQONMTPEQRKENYLCDITYVTNSELGFDYLRDNLATESVEELVLR
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STESAEFESIYKLKVTIVPTNKPMIRKDESDVVFKAVNGKWRAVVVEISRMHKTGRAV
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.15946,
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/ note = "encodes putative SecA-type chloroplast protein

transport factor; gene model last edited on 26 Mar 9;

/evidence = not experimental

complement (join (14442. .14579,14663. .14902,14991. ...

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/gene = "T7B11.6"

/note = "functional catalog ID=06.04; functional catal
                                   identical
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                                                                                                                                                                                                                                                           /translation="MRGVTPINPOKKIEADSNPVKESDYYEGERLTHL:
SKLSNVNSLPEKIWLKKQIAIGINEVTRVLERMNPNNTSDQOQNPKQL
PRMLTKHIPNLAASRNVPVLYVRDNKRASLRLGELVKLKTALAIGIKA
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                                     ated protein; idea number AF104919;
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product="putative RNaseP-associated
protein_id="AAD22641.1"
db_xref="GI:4558548"
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Mismatches
         /gene="T7B11.5"
/note="encodes RNaseP-associated/
T15B16.20, GenBank accession numb
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14020. .14244)
/gene="T7B11.5"
/note="identical to T15B16.20
AF104919; functional catalog
                                                      SenBank accession
on 3 Mar 99"
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product="putative SecA-ty
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13454,13566.
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xref="GI:4558549"
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Direct Submission

Direct Submission

Direct Submission

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevan@bbsrc.ac.uk

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/

this fragment has an overlap with ATCHRIV4 at the 5' end and an

coverlap with ATCHRIV6 at the 3' end.

I. 198220

I. 198220
16-MAR-2000
                                                                                                                                                                Tracheophyta;
                                                                                                                                                                                                   Spiegel, L.A., Huang, E.N., Nascimento, L.U., de la Bastide, M., Vil, D.M., Preston, R.R., Matero, A., Shah, R., O'Shaughnessy, A., Rodriguez, M., Shekher, M., Schutz, K., See, L.H., Swaby, I., Unpublished
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                                                                                                                                                                                                                                                                                                                                                                             Tracheophyta;
Pinus; Pinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 ATTGAGGCCATGGCGCATCTCCCATGTGACTACGGGTCTATTGAAATGGGGATTCGTGG
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                             TGAAGACACGITTGITGCAAAGITAAAATGGAAAITGITGTCAGCAAAGACCAGGITGA
                                                               ATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGAGAGATTGGTGATGGCAAGAT
                                                                                                                    TTTTGTTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGAGCGTGGGGAGAAAGC
                                                                                                                                   ATTCTTGACTCCCATCTCCGATGTTATAAGAGTTCGCACTGGTGAACGGGGGAGAAAGGC
         and
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                                                                                                                                                                                                                                                                                                                                                                                                                                      adult Maritime pine
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                                                                                                                                                                                                                                                                                             (alb gene)
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                                                                                                                                                                                                                                                                                 1085 bp mRNA
PII-like protein
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Pred, No. 2.3e-39;
); Mismatches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pinus pinaster'
/mol_type="mRNA"
/db xref="taxon:71647"
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dev_stage="adult tr
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1. .1085
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glb gene; PII-like protein
Pinus pinaster
Pinus pinaster
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ilarity 70.9%;
Conservative (
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42. .773
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Submission
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A PII-like p
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/product="PII-like protein"
/protein_id="AAR14689.1"
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mplete cds.
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                                            804
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Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 947)
Walch-Liu,P., Roemheld,V. and von Wiren,N.
A PII-like protein in tomato
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TIAAC
                                          TGTACATGAATTATGCAGAAACATCTGTCCTGGTTCTCAGACATCGAAACTCTGTTCCTA
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                                                        TGTACATGAATTATGCAGAAACATCTGTCCTGGTTCTCAGACATOGAAACTCTGT
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TAATAATGAATGGAGTCTGTTTTGGTTTCATGTTGAATCGATCAAGATGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCA
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(GLB1) mRNA,
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Pred. No. 8.9e-48;
0; Mismatches 120;
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                                                                                                                                                                                             AY442185
Lycopersicon esculentum PII-like protein AY442185
AY442185.1 GI:38231569
                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:4081"
1. -947
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larity 72.5%;
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Agrobiological Sciences Rice Full-Length cDNA Project Team:,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundarion of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, H., Kobayashi, M., Xie, Q., Lu, M.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Miura, J.,
Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Salto, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sosino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 331 (5631), 376-379 (2003)
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Sakai,K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK068407.1 GI:32978425
FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hotta, I., Iida, Y., Ishikawa, M., Imamura, K., Horta, I., Iida, Y., Ishikawa, M., Itoh, M., Kagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doi, K.,
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ACGG
                         GAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGAT
                                                                                                                                                                                                                           TAAAGATCAGGTAGAAGCAGTAATTGATGCAATCATTGATGAGGCAAGAACTGGAGAAAT
                                                                                                                                                                                                                                                                                  TGGTGATGGCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAGGTGA
                                                                                                                                                                                                                                                                                                             GTTCTCGGAAGACAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAA
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Oryza sativa (japonica cultivar-group) cDNA clone:J013149B08,
 TGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGAC
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PUBMED
REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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KEYWORDS
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Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, T., Shishiki, T., Tagami, M., Tagami, Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

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Tel:81-29-838-7007, Fax:81-29-838-7007)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URE: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Bazuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Sugiyama,A., Matsubara,K. and Murakami,K.
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and Genome Science Laboratory in Riken: Genomic Sciences Center
and Genome Science Laboratory in Riken: Wida,S., Harangaki,T.,
Akimura,T., Hori,F., Iida,J., Imamura,K., Harangaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H.,
Sasaki,D., Sato,K., Sakai,K., Numasaki,R., Ohno,M., Osato,N.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
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Pred. No. 6.4e-37;
); Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa.
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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ramamoco, m.

Pals Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,

Pujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Fujimura, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,

Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,

Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Sugiyama, A., Matsubara, K. and Murakami, K.

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Akimura, T., Arakawa, T., Carninci, F., Fukuda, S., Hanagaki, T.,

Akimura, T., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hara, A., Hashizume, W., Hayashida, K., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,

Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kawai, J.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Osato, N.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,

Sasaki, D., Sato, K., Shibata, K., Sahazume, N., Sano, H.,

Sasaki, D., Sato, K., Shibata, K., Sahazume, N., Sano, H.,

Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,

Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,

Yasunishi, A. and Hayashizaki, Y.
                        CDNA clones from japonica
                                                                          URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
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Pred. No. 6.4e-37;
); Mismatches 106;
81-29-838-7007, Fax:81-29-838-7007)
clone is one of the 28K full-length
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db xref="taxon:39947"
clone="J023070H02"
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Job time: 2419.14 secs
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                                                                                                                                                                                                 Obneda, E., Yamamoto, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283
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Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
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Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
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Laboratory of Gene Expression; 2-1-2 Kannondai, Ts
305-8602, Japan (E-mail:8kikuchi@nias.affrc.go.jp,
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## ALIGNMENTS

CDNA. BP 817 Arabidopsis thaliana P-PII entry) AAF58581 standard; cDNA; (first AAF58581; AAF58581 

Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening; ss.

thaliana Arabidopsis

US6177275-B1.

23-JAN-2001

97US-00899330. 23-JUL-1997; 96US-0022328P 24-JUL-1996;

(UYNY ) UNIV NEW YORK STATE.

Hsieh M;

Lam H,

Cornzzi GM,

WPI; 2001-158572/16 P-PSDB; AAB69495.

assimilation, Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 2; Fig 12; 35pp; English.

clones The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic closwith the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms
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transgenic plant; herbicide screening;
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                                                                                                                                                                                                                                                           Novel P-PII genes capable of regulating plant nitrogen useful for transgenic plant production, and as probes 1 additional genomic clones having P-PII gene promoters.
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTAGTGATGAAATGGTCGACGCGGTAATTGAGTCAATTACACGTGTGGCAAGCACTGGA
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                                                                                                                                                                                                           Acinetobacter baumannii protein #1311
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                                                                                                                                                                                                                                       ds; gene; Acinetobacter baumannii; bacterial vaccine; plant biocontrol agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising of a combination of 41 nucleic acid molecules (see AAF28514-AAF28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as otitis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
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Pred. No. 7.1e-15;
0; Mismatches 132;
                                                                                                                                                                              Genomic library; bacteria; human upper airway; bronchopulmonary; endocarditis; meningitis; ss
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               The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences as sources of probes and primers for detecting the genome of P. lumi and related species; to study polymorphisms; for gene analysis as detection/amplification of the genes. Antibodies [Ab] raised again polypeptides encoded by the genes are used for detection/identificarry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in animals or microorganisms other than P. luminescens and are able
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are sensitive to P. luminescens-encource communities are as this proteins are as the properticides. Other uses of the genes and the proteins are as tactors and for identifying targets of human diseases for which factors and for identifying targets of human diseases for which luminescens is a model (particularly plague and whooping cough).
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manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
                                                                                                              256 ACAAGGIGGAAGCAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTACTGA
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antigen; vaccine; diagnosis; infection; antibacterial; identifica
Meningococcus B; MenB; ds.
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meninglitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81301 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polymucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament for in the manufacture of a medicament) for treating, preventing or diagnosing infection due to Neisserial bacteria. For example, some of the identification of sequences from the bacterium pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more
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CA922829 EST640547
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BE239550 EST403599
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BI932913 EST549999
BE645522 NF036F08E
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1 (bases 1 to 566)
Seki,M., Narusaka,M., Ishida,J., Kawiya,A., Satou,M., Nakajima,Nono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki, and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
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AU236084 RAFL14 Arabidopsis thaliana cDmRNA sequence.
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An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
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33-E9570-012-004-A09-T7R MPIZ-ADIS-012 Arabidopsis thaliaclone MPIZp769A094Q 5-PRIME, mRNA sequence.
CB261070
CB261070.1 GI:32885843
EST.
Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                Score 499.6; DB 9;
Pred. No. 4.8e-94;
); Mismatches 6;
                                                                                             thaliana
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                                                                                                                                                                    Site
                                                                                                                       /clone="RAFL14-63-K15"
/tissue_type="root"
/lab_host="DH10B"
/clone_lib="RAFL14"
/note="Site_1: BamH1; S
                                                                                            /organism="Arabidopsis
/mol_type="mRNA"
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                                                                       Location/Qualifiers
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larity 98.2%;
Conservative
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ACCESSION VERSION KEYWORDS

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/db_xref="GABI:589834"
/db_xref="GABI:589834"
/db_xref="MPIZP69A0940"
/tione="MPIZP69A0940"
/tissue_type="whole plant"
/dev_stage="adult plant, mixed stresses"
/lab_host="E. coli XI1-Blue MRF"
/foloe_lib="WPIZ-ADIS-012"
/note="Vector: pSPCNT1; Site 1: SalI; Site 2: NotI; cDNA
library from Arabidopsis thaTiana, accession Landsberg
erecta; six weeks old total plants were treated for 24
hours with different stresses, (1) at 4M-0 C in the dark,
(2), at 37 Grad C in the dark, (3) lying in the lab after
removing from soil, (4) in the greenhouse after wounding
leaves with a foreceps, (5) in the lab watering with a 150
mM Nacl solution, (6) at 26 Grad C in the light/UV; equal
quantities of stressed plant material were pooled; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites SalI-NotI,
primer sites and orientation:
T7-SalI-CCACGCGTCG-Sprime-CDNA-polyA-CC-NotI-SP6; Note:
Sequencing granted in the context of the GABI Arabidopsis
Verbund I: Genetic Diversity, 'Establishment of
high-efficiency SNP-based mapping tools and development of
methods for genome-wide mutation detection' PI: Bernd
Weisshaar Sequence submission managed by RZPD/GABI-Primary
database: http://gabi.rzpd.de. This clone is available
information"
information"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Eukaryota; Viridiplantae; Streptophyta; Englished in Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 549)

Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.

Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)

E 22683290

D 12799357

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851
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Pred. No. 8.6e-94;
0; Mismatches 11;
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/mol_type="mRNA"
/cultivar="Landsberg erecta (Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 549 Std Error: 0.00
Plate: 4 row: A column: 09
Seg primer: T7R; CTAATACGACTCACTATAGGGA
Location/Qualifiers
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illarity 97.6%;
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AUTHORS
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KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 685)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
Genoplante
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This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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TCGTGTTTTACCTGTCGTTAGTGCCCAAATATCTTCTGATTATATTCCAGACTC-GAAAT
                                                                                                                                                             Gaps
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BN25,060G17F011129 BN25 Brassica napus cDNA clone BN25060G17
                                     AGATGGAAATCGTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATT
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9.5e-86;
nes 84;
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/wol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN25060G17"
/tissue_type="seed"
/clone_lib="BN25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 459.6; Pred. No. 9.5e
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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illarity 85.9%;
Conservative (
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CD825321.1
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AUTHORS
TITLE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 732)
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Jet neuf"
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Genoplante, a major partnership
Unpublished (2003)
Contact: Genoplante
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/clone="BN25040D05"
/tissue type="seed"
/clone lib="BN25"
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BN25.040D05F011026 BN25 B
sequence.
CD820903
CD820903.1 GI:32502843
EST.
Brassica napus (rape)
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Tel: 33 1 69 47 54 00
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This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
1. .745
                                                                                                                                                                                                                                                     TGTCGTTAGTGCCCAAATATCTTCTGATTATTTCCAGACTCGAAATTTTACAAGGTGGA
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                                                                                                                                                                                 Length
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                                                                                                                                                                                  DB 14;
                                                                                                                                                                                 Score 456.8; DB 14
Pred. No. 3.5e-85;
; Mismatches 117;
                                                                                               /organism="Brassica napus"
/wol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN20047L06"
/tissue_type="seed"
/clone_lib="BN20"
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                                                                                                                                                                                 55.9%;
ilarity 82.0%;
Conservative
Unpublished (2003)
Contact: Genoplante
Genoplante
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Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudico
rosids; eurosids II; Brassicales; Brassicaceae; Brassica
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                     33;
   732
   Length
                    Indels
  Score 458.8; DB 14;
Pred. No. 1.4e-85;
; Mismatches 112;
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   56.2%;
Similarity 80.8%;
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BN20.047L06F011226 E
sequence.
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CD819046.1 GI:32500
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Best Local Similarity 96.9%;
Matches 409; Conservative
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AU226889
AU226889.1 GI
EST.
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                                                                                                 Brassica napus
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
1 (bases 1 to 669)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG---AACATTGCTTTCTCTGATTGCATTTCGATTTGTTCTGGATTCAGACATTCCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCTTGCCTCGATTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTC
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                           linear
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1.4e-84;
whes 85;
                        669 bp mRNP
Brassica napus
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Pred. No. 1.4e-
0; Mismatches
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Genoplante, a major partnership
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                     /cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN25045G20"
/tissue_type="seed"
/clone_lib="BN25"
                                                                                                                                                                                                               91025
                                                                                                                                                                                                                                                                                                             type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                                                                                            93, rue Henri Rochefort
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                      CD822497
BN25.045G20F020108 BN25
                                                                 GI:32504437
                                                                                      Brassica napus (rape)
Brassica napus
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larity 85.6%;
Conservative
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EST.
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                                              sequence.
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 451)

2 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Layashizaki,Y. and Shinozaki,X.

Large scale analysis of Arabidopsis full-length cDNA

Wuramatsu,M., Hayashizaki,Y. and Shinozaki,X.

Large scale analysis of Arabidopsis full-length cDNA

Contact: Motoaki Seki

Unpublished (2002)

Contact: Motoaki Seki

Plant Functional Genomics Research Group

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Fax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and Xhol was ligated to modified Lambda Fic.1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Euclicots;
Spermatophyta; Magnoliophyta; euclicotyledons; core euclicots;
Spermatophyta; Magnoliophyta; euclicotyledons; core euclicots;
Spermatophyta; Magnoliophyta; euclicotyledons; core euclicots;
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/tissue_type="root"
/lab_host="DH108"
/clone_lib="RAFL14"
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Pred. No. 6.3e-67;
0; Mismatches 9;
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       AG--CGTGGGGAGAAAGCAGAGATGACTGGTGATATGCTTTCACCGTCTTA
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                                                            TTTTCATTTCGGTCTCTAGATTCTGC
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Department of Fruit Science
Southwest Missouri State University-Mountain Grove
9740 Red Spring Road, Mountain Grove, MO 65711-2999, USJ
Tel: 417 926 6646
Email: weq070f@smsu.edu
Insert Length: 782 Std Brror: 0.00
Plate: VAN-Baker-1-12 row: F column: 06
Seq primer: T3 PRIMER
High quality sequence stop: 782
POLYA=No.
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Hou, H.S., Phanikanth, T.V., Kovacs, L. and Qiu, W.P.
Expressed sequence tags of young leaf tissues of
disease-resistant Vitis aestivalis var. Norton
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                        Vitis aestivalis
Eukaryota, Viridiplantae, Streptophyta, Embryo
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids, Vitaceae, Vitis.
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V-B-112F06 VAN-Baker-1 Vitis aestivalis
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/lab_host="XL10-Gold E .coli"
/clone_lib="VAN-Baker-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Vitis aestivalis"
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                                                           AACAGAGCTCAAGAATGGTTTTTTT
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Vitis aestivalis
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Length 782;

DB 14;

Score 270.6;

33.1%;

Query Match

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                                                          CTTTCTCTGATTGCATTTGTTCTGGATTCAGACATTCCCGACCATCTTGCCTCG
                                                                                                   crcrcaradacrdcarrrdarccaccccarcrcaagarrcrdaaaarrrccagrira
                                                                                                                                                <u>AFTTGGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCAAA</u>
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I (bases 1 to 723)

Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu, F., Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grimplet, Hamdi, S., Romieu, C. and Terrier, N. Generation of Expressed Sequence Tag from Grape Berry (Bkin, por seeds) at Various Developmental Stages

Unpublished (2002)

Contact: Romieu C.

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Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
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BST 6939 Ripening Grape berries Lambda Zap II L. vinifera cDNA clone RT093C02 3', mRNA sequence.
BQ798001.1 GI:22012967

EST.
Vitis vinifera
  2.le-46;
les 134;
  Pred. No. 2.10
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/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
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/clone="RT093C02"
/dev_stage="ripening stage"
/clone lib="Ripening Grape berries Lambda Zap II Libra/
/clone lib="Ripening Grape berries Lambda Zap II Libra/
/note="Organ: Fruit; Vector: Lambda Zap II; Site 1: Ex
RI; Site 2: XhoI; Oriented library, construction descring Generation of ESTs from grape Berry (skin, pulp or in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier, N., Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol.
(12): 1575-83 2001"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
asterids; lamiids; Lamiales; Antirrhinaceae; Antirrhineae;
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AJ558383
AJ558383.1 GI:31660955
EST.
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                                                                                                                                                           DB 13;
                                                                                                                                                    Score 262.8; DB 13;
Pred. No. 9.3e-45;
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829,
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/clone="018_1_07_f22"
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Antirrhinum majus
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Zachgo,S., Stueber,K., SaedAntirrhinum EST collection Unpublished (2003)
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ilarity 76.8%;
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant
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VandenBosch, K., Endre, G., Silverstein, K., TowndenBosch, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 6K unigene set: cDN re-arrayed from various libraries
Unpublished (2002)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Par
Tel: 612 624 2755
Fax: 612 625 1738
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Alias Clone pMHRP-28F3
TIGR sequence name: MTUCF91TV
More information is available at: www.med
Seq primer: (gtA AtA CgA CtC ACt AtA ggg
Location/Qualifiers
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                                                                    Score 252.8; DB Pred. No. 1.1e-42
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348; Conser
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                            /dev_stage="various stages"
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/lab_host="XLOLR"
/clone lib="MTUS"
/clone lib="MTUS"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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ESTs from developing reproductive tissues of Mediuppublished (2001)
                                                                                                                                                                                                                  Indels
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USDA/ARS Children's Nutrition Research Center
                                                                                                                                                                                         DB 14;
                                                                                                                                                                                        Score 249.6; DB 14,
Pred. No. 5e-42;
J; Mismatches 139;
db_xrel=__carc....
|clone="MTUS-58H7"
|tissue_type="mixed_tissues"
|tissue_type="mixed_tissues"
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politimation.

/clone_lib="GESD"
/clone_lib="GESD"
/note="Vector: pBluescript SK-; Site_l: EcoRI; Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA-
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propogated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TETTACCTGTCGTTAGTGCCCGAATATCTTCTGATTATATTCCAGACTCGAAATTTTACA
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Pred. No. 1.2e-41;
0; Mismatches 167;
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                                77030-2600,
                                                                                                                                                                                                           TIGE sequence name: MTPAP50TK
More information is available at: www.m.
Seq primer: SKmod (CTA gAA CTA gtg gAT C
Location/Qualifiers
1. 714
/organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beeds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="immature seeds
/dev stage="Immature seeds,
pollination"
                                  Ϋ́Х
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:3880"
clone="pgESD9J4"
                                       Houston,
Medicine
                                                                                                                                           mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
cultivar="A17"
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Baylor College of Me
1100 Bates Street, I
Tel: 713-798-7044
Fax: 713-798-7078
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613 bp mRNA linear EST 18-MAY-2001
TAMU Lycopersicon esculentum cDNA clone
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TGGGAATTCGTGGTGTCACTGTATCTGATGTCAAGGGGTTTGGTGCTCAGGGTGGCTCAA
                        COGAGAGACACGGTGTGTTGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGG
                                      AAGAGGCAGGGAGGCTCCGAATTTTCTGAAGACAATTTTGTTGCCAAAGTTAAAATGG
                                                                                           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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                                                                                                                                                                                                            577
                                                                                                                                                                                    603
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                                                                                                                                                                                                      esculentum"
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120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 245; DB 9;
Pred. No. 5.1e-41,
0; Mismatches 12(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="callus"
/dev_stage="25-40 days old
/lab_host="XL1-Blue_MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon e:
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEC36D8"
                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                AW035791
EST281945 tomato callus, T cLEC36D8, mRNA sequence.
AW035791
AW035791.1 GI:5894547
EST.
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Best Local Similarity 72.5%;
Matches 317; Conservative
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AUTHORS
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SOURCE
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AW035791
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                                                                                                                                                                             Tracheophyta;
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                                                                                                                                                                                                                                            Hansen, T.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                     Linear EST 12
clone pMHRP-28F3,
                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicot
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Tri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 AAGITGAAGCCATTCTCAGGCCATGGAGAATCCCTCAGGTTTCTTCGGGTTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITIACCIGICGITAGIGCCCAAATAICIECIGAITAIATICCAGACICGAAAI
                                                                                                                                                                                                              1 (bases 1 to 597)
Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Hanse Holt, I.E., Cho, J. and Fraser, C.M.
ESTS from phosphate-starved roots of Medicago truncatula Unpublished (2000)
Contact: Maria J. Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                           Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, US
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N265417e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ပ္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 246.6; DB 10;
Pred. No. 2.4e-41;
); Mismatches 99;
                                                                     BE239550
EST403599 MHRP- Medicago truncatula cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /crganism="Medicago truncatula"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pMHRP-28F3"
/tissue_type="roots"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                  TIGR sequence name:MTHAC26TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod {CTA gAA CTA gAT
Location/Qualifiers
    GAATTGATAACAATGATGTATTTTT
                                                                                                                                                   (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            xref="taxon:3880"
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ilarity 75.6%;
Conservative (
                                                                                                                         GI:9055733
                                                                                                                                                   truncatula
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Medicago truncatula
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BE239550
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Best Local
       652
                                                                                    DEFINITION
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VERSION
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AUTHORS
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JOURNAL
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                                             RESULT 13
BE239550
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/db_xref="taxon:4081"
/clone="cTOC22G23"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/note="Vector: pBluescript SK{-}; Site_1: EcoRI; Site_2:
xhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8-OCT-2001
sicon
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TA496).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tracheophyta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyti

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 702)

van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,

Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,

Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics
                                                                                                                                                                                                                                                                             AATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGGTGTTACTGTTTCTGA
                                                                                                                             GGAAGACAAATTIGITIGCTAAAGTTAAGATGGAAATCGTTGTTAAGAAAGACCAAGTGGA
                                                                                                                                                                                                                             TGAAGACACGTTTGTTGCAAAAGTTAAAATGGAAATTGTTGTCAGCAAAGACCAGGTTGA
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
Institute
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EST552012 tomato flower, 8 mm to preanthesis buds Lycoesculentum cDNA clone cTOC22G23 5' end, mRNA sequence.
BI932123.1 GI:16246595
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Unknown.
Unclassified.

( bases 1 to 897)

Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 14 23-JAN-2001;
Location/Qualifiers score DNA to the score of the total **ALIGNMENTS** 897 bp US 6177275 AR125590
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Hsieh, M.H., Lam, H.M., van de Loo, F.J.
Direct Submission
Submitted (29-SEP-1998) Biology, New
Washington Square East, New York, NY
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/db_xref="taxon:3988"
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/organism="Medicago s'
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larity 72.0%;
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Garcia-Ibilcieta, D.
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CCAGGTTGAGGATGTTATAGAAAATCATTGAGGAGGCAAGAACTGGAGAGTTGGAGA
                                    CGGCAAGATTTTCTTGCTGCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGCGGGG
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Mismatches 0;
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.

Plant nitrogen regulatory P-PII genes

Patent: US 6177275-A 16 23-JAN-2001;

Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Submitted (22-FEB-2001) Molecular Biology 1
University, Corner of Knox and College, Las
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Pred. No. 1.8e-63;
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codon_start=1
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VSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKMRIVVKKDQVESVINTIIEGARTGEI
GDGKIFVLPVSDVIRVRTGERGEKAEKMTGDMLSPS*
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 844)
Hsieh,M.H., Lam,H.M., van de Loo,F.J. and Coruzzi,G.
A PII-like protein in Arabidopsis: putative role in nitrogen sensing
                                                                                                 AGATTGGAGACGCCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTG
                                                GAGGTGTTACTGTTTCTGATGTTCGAGGTTTTGGTGCTCAAGGTGGTTCAACTGAGAGGC
                                                             CCTCGGCTTTGCTAAAATTGGTATTC
             CAATTGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTC
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Pred. No. 4.6e-60;
0; Mismatches 171;
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Hsieh, M.H., Lam, H.M., van de Loo, F.J.
Direct Submission
Submitted (29-SEP-1998) Biology, New
Washington Square East, New York, NY
Location/Qualifiers
  CAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTT
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Matches 402; Conservative
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Pred. No. 4.6e-60;
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Coruzzi, G.M., Lam, H.-M. and Hsieh, M.-H
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 13 23-JAN-2001;
Location/Qualifiers
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/organism="Arabidopsis t/mol_type="unassigned DN/db_xref="taxon:3702"
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 15 23-JAN-2001;
Location/Qualifiers
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VSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKMBIVVKKDQVESVINTIIEGARTGEI
GDGKIFVLPVSDVIRVRTGERGBKAEKMTGDMLSPS"
      The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Chan, M.M., Chang, C.M., Dale, J.M., Hsuan, V.W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J. Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C. Yamada, K., Yu, G., Yuan, S., Davis, R.W., Theologis, A., and
                                                                                                                                                                           Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
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/mol_type="mRNA"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 591)
Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Cnodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
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Chan,M.M., Chang,C.H., Dale,J.M., Hayashizaki,Y., Hsuan,V.W.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M.
Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K.,
Yu,G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and
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Submitted (14-MAR-2003) Salk Institute Genomic Analysis L.
(SIGNAL), Plant Biology Laboratory, The Salk Institute fo
Biological Studies, 10010 N. Torrey Pines Road, La Jolla,
                                                                                                            CTCGATITIGGICACAAAGICACCGAGIAAIAACAGICGIGIITITACCIGICGIIA
                                     CAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTC
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AUTHORS
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The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team:,
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Dobi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., Rikens,
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
                                                                        481 AGTCATTGCCAAGATAATTGAAGAGGCAAGAACTGGTGAAATAGGTGATGGAAAGATATT
                                                                                                                                                                                                                         GAGGATGATGGGGGGCATGCTGATATGTCCTCTGCATTATCAACTTCTTGAGCGGCAA
                                                                                                                                                                              GAGGATGACAGGAGGCGATCTGACATGAGTACTTCTGCTTGACTGTGACCAGCAA
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Track
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
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Science 301 (5631), 376-379 (2003)
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(japonica cultivar-group)
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VRGFGAQGGLTERQAGSEFSEDTFVAKVKMEIVVSKDQVEGVIAKIIERARTGEIGDG
KIFLTPISDVIRVRTGERGEKAERMMGGHADMSSALSTS"
                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 947)
Walch-Liu, P., Roemheld, V. and von Wiren, N.
A PII-like protein in tomato
Unpublished
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2 (bases 1 to 947)
Walch-Liu, P., Roembeld, V. and von WireL., L., P., Roembeld, V. and von WireL., L.

Direct Submission
Submitted (17-OCT-2003) Institute of Plant Nutrition, Submitted (17-OCT-2003) Institute of Plant Nutrition, University, Fruwirthstr. 20, Stuttgart 70593, Germany Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                      linear PJ
(GLB1) mRNA,
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/product="PII-like protein'
/protein_id="AAR14689.1"
/db_xref="GI:38231570"
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/mol_type="mRNA"
/db_xref="taxon:4081"
                                                                           GAGAAAGCAGAGAAGATGACTGGTG
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                                                                                                                              zaki,J.,
.., Namiki,T.,
Shishiki,T. ?
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                                                                                        URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T
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  Gene Expression; 2-1-2 Kannondai, Ts
in (E-mail:skikuchi@nias.affrc.go.jp,
-7007, Fax:81-29-838-7007)
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Ishikawa, M., Yamada, H.,
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FAIS Genome Sequencing
Laboratory C. 305-8602, Japan (E-mai
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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11-0CT-2003

PLN

(glb gene)

1085 bp mRNA for PII-like protein

Pinus pinaster mRNA

DEFINITION

LOCUS

RESULT 13 PPI489604 PPI489604

linear

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/translation="MAAHLPLFVKGSIFSLPSSTSTSSSCTYSSISHTAASPGFHSSP
AAANKSVKLGTMQRMDGVRSVKHRMTSLHAKMEKRQQIKASAQAPNGTNTHPDYVPEA
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SKVKMEIVVSKDQVEAVIDAIIDEARTGEIGDGKIFVVPVADVIRVRTGERDLKPERM
AGGDQRYLQVYIKRLQTATKSLLAL"
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Pinus; Pinus
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Pinus pinaster
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
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Pred. No. 1.8e-42;
); Mismatches 101;
                                                                                                                       adult
                                                                                                                                                                                                                                                                                                                                            /gene="glb"
42. .773
/gene="glb"
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                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                             1. .1085

/organism="Pinus pinaster"

/mol_type="mRNA"

/db_xref="taxon:71647"

/tissue_type="xylem"

/dev_stage="adult tree"

1. .1085
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                                                                                             Carton, F.J.
A PII-like protein from xylem Unpublished
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glb gene; PII-like protein
Pinus pinaster
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Canton, F.J.
Direct Submission
Submitted (11-JUN-2002)
Biochemistry, Faculty of SPAIN
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RYRGSEYTVEFLQKLKVEIVVDDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRI
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Characterization of the glnB gene product of Nostoc punct
strain ATCC 29133: glnB or the PII protein may be essent:
Microbiology 144 (Pt 6), 1537-1547 (1998)
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae;
1 (bases 1 to 686)
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Davis, CA 95616,
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Pred. No. 1.2e-15
0; Mismatches 12
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organism="Nostoc punctiforme"
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) gene,
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Hanson, T.E. and Meeks, J.C.
Direct Submission
Submitted (05-AUG-1997) Section of
California, One Shields Avenue, Da
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="AAC26348.1"
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                                   (glnB)
                                                                                                                                                                                                                                                                                                                                                                                               /function="putative I
/codon start=1
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Nostoc punctiforme PII
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/db_xref="GOA:Q9L422"
/db_xref="GOA:Q9L422"
/db_xref="SPTREMBL:Q9L422"
/db_xref="SPTREMBL:Q9L422"
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RYRGSEYTVEFLQKLKVEIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRI
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/gene="glnB"
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glnB gene; PII protein.
Nostoc sp. PCC 7120 (Anabaena s)
Nostoc sp. PCC 7120
Bacteria; Cyanobacteria; Nostoc
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residues 2124099041 3373863 seqs, Searched:

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## ALIGNMENTS

Castor bean; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening; BP AAF58582 standard; cDNA; 897 Ricinus communis P-PII cDNA. entry) (first 23-APR-2001 AAF58582; RESULT 1 **AAF58582** 

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96US-002232BP. 97US-00899330 communis US6177275-B1. 23-JUL-1997; 24-JUL-1996; 23-JAN-2001 Ricinus 

Hsieh M; Lam H, WPI; 2001-158572/16 P-PSDB; AAB69496. Coruzzi GM,

(UNNY ) UNIV NEW YORK STATE.

Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

Claim 2; Fig 13; 35pp; English.

The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

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                                          : nitrogen regulatory gene; F
transgenic plant; herbicide
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                                          Castor bean; PII; plant nitrogen nitrogen assimilation; transgenion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-158572/16
P-PSDB; AAB69495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clawith the promoters of P-PII genes. P-PII promoters are light- and/or
                                                          AGCGG
                                                          GACGGCAAGATTTTCTTGCTGCCTGTTTCAGATGTAATAAGAGTCCGCACTGGTGAGGCGG
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                                                                                                                  643
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                                                                                                                                                                                                                                                                                                                                     PII; plant nitrogen regulatory gene; P-PII; transgenic plant; herbicide screening; ss.
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Pred. No. 7.7e-61;
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69.8%;
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P-PSDB; AAB69495.
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transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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Pred. No. 1.5e-60;
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                                                                                     588 BP; 164 A; 105
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                                                                                                                                  condition to which a plant cell has been exposincreased tolerance to these abiotic stresses
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165;
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illarity 70.3%;
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2001US-0300111P
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producing plants with
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26-JAN-2001;
22-JUN-2001;
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                                                        2; DB 2;
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tis; meningitis; s
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specification e.g. is useful for aidentifying diagnostic and the compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the baciflora of human upper airways. M. catarrhalis is known to cause a localised infections such as otitis media, sinusitis and bronchol infection and life-threatening, systemic diseases including endo
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for diagnosing a bacterial disease, as components of antibacte
vaccines, as targets for antibacterial drugs, or as biocontrol
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                            The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for protein.

The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
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                                                                                            The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences as sources of probes and primers for detecting the genome of P. lumiand related species; to study polymorphisms; for gene analysis and detection/amplification of the genes. Antibodies {Ab} raised again polypeptides encoded by the genes are used for detection/identificarry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in animals or microorganisms other than P. luminescens and are able response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for the secons.
                                          lence of Photorhabdus luminescens and encoded polypep
as therapeutic antimicrobials and agricultural pesti
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                                                                                                                                                                                                                         recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicit genes, proteins, vectors containing the genes and Ab are also us therapeutically (to treat microbial infection by bacteria or fur
                                                                                                                                                                                                                                                                  are sensitive to P. luminescens-encoded toxins or antibiotics) a biopesticides. Other uses of the genes and the proteins are as a factors and for identifying targets of human diseases for which luminescens is a model (particularly plague and whooping cough). sequence represents one of the isolated P. luminescens genes
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77 C; 123 G;
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Meningococcus B; MenB; ds.
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30-APR-1999;
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proteins

The present invention describes methods of obtaining immunogenic from Neisseria genomic sequences. AAA81453 to AAA82414 represent

466-471; 1760pp; English

Page

other

ch can and ot

Isolated nucleotide sequences of Neisseria meningitidis which in the diagnosis and treatment of N. meningitidis infection and Neisserial infections, for example, N.gonorrhoea.

Pizza M;

Rappuoli R,

WPI; 2000-318079/27.

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specifically claimed Neisseria meningitidis genomic DNA sequences;
AAA81260 to AAA81303 and AAB25620 to AAA815563 represent Neisseria DNA
sequences and their corresponding proteins; AAA81254 to AAA81259 and
AAA81304 to AAA81321 represent PCF primers used in the isolation of
Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent
Neisseria meningitidis MenB polymucleotide ORF sequences, which are all
sequences, protein sequences, and antibodies against them, can be used in
the manufacture of a composition. The composition can be used as a
medicament (or in the manufacture of a medicament) for treating,
preventing or diagnosing infection due to Neisserial bacteria. For
example, some of the identified proteins could be components of vaccines
against Meningococcus B; against all serotypes; and/or against all
coganism-specific probes. Attempts to make efficacious Meningococcus B
vaccines have failed mainly due to antigen tolerance. Multivalent
vaccines have also been tried but none have successfully overcome
that may be presumed targets for the immune system and which are not
variable variable or at least more conserved than other more
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T15252

CN Cr8852 lambdaZAPST Ricinus communis cDNA clone pcr8852 similar to nitrogen-regulatory protein, mRNA sequence.

N T15252

T15252.1 GI:14190796

EST.

Ricinus communis (castor bean)

SM Ricinus communis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalypheae; Ricinus.

E vandeLoo, F.J., Turner, S. and Somerville, C.

Expressed sequence tags from developing castor seeds

L Cantact: Somerville CR

Carnegie Institution

Carnegie Institution, 290 Panama St, Stanford, CA 94305

Tel: 4153251521

Email: crs@andrew.stanford.edu

Seq primer: T3.
BI311072 EST531282
CA922829 EST640547
BF645522 NF036F08E
CF920467 GMThRww3-
C81819 Citr
BE823431 GM700019B
BM113473 EST561009
BI932336 EST55225
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BI932123 EST552012
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CD819046 BN20.047L
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                                                                                                        /note="Vector: lambdaZAPII; Site I: EcoRI; Site 2: XhoI Poly(A) + RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. CDNA was synthesized and cloned into lambdaZAPII accordito the instructions of the manufacturer (Stratagene): synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate. "
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Hou, H.S., Phanikanth, T.V., Kovacs, L. and Qiu, W.P. Expressed sequence tags of young leaf tissues of disease-resistant Vitis aestivalis var. Norton Unpublished (2003)
Contact: Wenping Qiu
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clone="pcrs852"
clone_lib="lambdaZAPST"
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 mol_type="mRNA"
strain="Baker 296"
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nilarity 95.5%;
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/clone="V-B-112F06"
/tissue_type="Leaf"
/dev_stage="Young leaf"
/dev_stage="Young leaf"
/lab_host="XL10-Gold E .coli"
/lab_host="XL10-Gold E .coli"
/clone_lib="VAN-Baker-1"
/note="Vector: pBluescript II SK (+) Phagemid; Site_1: Xho
I; Site_2: EcoR I; VAN-Baker-1 is a cDNA library of Norton
grape young leaves (Vitis. aestivalis var. Norton). Norton
grape young leaves (Vitis. aestivalis var. Norton). The cDNA synthesis and library construction was performed
according to the instruction manual for pBluescript II XR
cDNA library construction kit provided by Stratagene."
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Southwest Missouri State University-Mountain Grove 9740 Red Spring Road, Mountain Grove, MO 65711-2999, USI Tel: 417 926 4105
Fax: 417 926 6646
Email: weq070f@smsu.edu
Insert Length: 782 Std Error: 0.00
Plate: VAN-Baker-1-12 row: F column: 06
Seg primer: T3 PRIMER
High quality sequence stop: 782
POLYA=No.
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                                                                                                                                                                                                                                                      /organism="Vitis aestivalis
/mol_type="mRNA"
/cultivar="Norton"
                                                                                                                                                                                                                                                                                                                         db xref="taxon:3605"
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GAGATTGTGGGGAAAGACCAGGTTGAAGCAGTAATTGACAAGATCAATGAGGTGGCA
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/clone="pMHRP-28F3"
/tissue_type="roots"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
/clone_lib="MHRRP-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N2
TIGR sequence name:MTHAC26TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT
Location/Qualifiers
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                                               AGAACTGGAGATTGGAGACGGCAAGATTTT
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Tel: 580-223-5810
Fax: 580-221-7380
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                                                                                                                                                                                               Tracheophyta
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Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGATCGTGGTTAGCAAAGACCAGGTTGAGGATGTTATAGAAAAATCATTGAGGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Fruit; Vector: Lambda Zap II LibraRI; Site 1: Edric Site 2: XhoI; Oriented library, construction describe Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier, N., Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. (12): 1575-83 2001."
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Grape berries Lambda Zap II
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II Library Vit.
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                                                                                                                                                                                               Embryophyta;
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2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-{0}4-99-61-28-62
Fax: 00-33-{0}4-99-61-28-57
Email: romieu@ensam.inra.fr
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Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; Vitaceae; Vitis.
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                                                                                             Zap
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Pred. No. 9.9e-38;
0; Mismatches 117;
                                                                                 mRNA
                                                                                            Lambda
                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Vitis vinifera"
/mol_type="mRNA"
/cultivar="Shiraz"
/db_xref="taxon:29760"
                                                                              BQ798001
EST 6939 Ripening Grape berries Lam vinifera cDNA clone RT093C02 3', mb BQ798001
BQ798001.1 GI:22012967
EST.
Vitis vinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="ripening
/clone_lib="Ripening
/note="Organ: Fruit;
RI; Site 2: XhoI; Ori
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ilarity 76.0%;
Conservative
          61
          CITGAGICCAAAIAI
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Best Local Similarity
Matches 371; Conser
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Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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XhoI; At the trifoliate stage, M. truncatula plants were
transplanted to phosphate-free sand and grown for a
further 30 days. During this period, they were fertilized
twice weekly with 1/2 Hoaglands solutions containing 20uM
potassium phosphate. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into the
Unizap XR vector from Stratagene and packaged using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 12-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                         304
                                                                                                                             63.1
                                                                                                                                                                                                24
44
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BST403599 MHRP- Medicago truncatula cDNA clone pMHRP-28F3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hansen, T.S.
                                                                                                                            GTCCGCACTGGTGAGCGGGTGATAAGGCTGAGAGGATGACAGGAGGCGATCTGACATG
                                 CITGCIGCCIGITICAGAIGIAATAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Hanse Holt, I.E., Cho, J. and Fraser, C.M.

ESTs from phosphate-starved roots of Medicago truncatula Unpublished (2000)

Contact: Maria J. Harrison

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73401, USA
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/clone lib="GESD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propogated in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GITTITGAITTICAGITTIGICCAGAGCITAGACAITCICGGITTICICACITTAAC
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                                                                                                                              /tissue_type="immature seeds"
/dev_stage="Immature seeds, 11
pollination"
/clone_lib="GESD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAGGATGACAGGAGGGCGATCTGAC
                                                                                             db_xref="taxon:3880"
clone="pgESD9J4"
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                                                     organism="Medicago
mol_type="mRNA"
cultivar="A17"
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nilarity 71.8%;
Conservative
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Best Local Similarity
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Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S.,
Cho, J. and Fraser, C.M.
ESTs from developing reproductive tissues of Medi
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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, US
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More information is available
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culture Medicago truncatula cDNA
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel 2002
Tel: 580 221 7302
Fax: 580 221 7380
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1. 612

/organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF036F08EC"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone lib="Elicited cell culture"
/clone lib="Sincited cell culture"
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Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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NF036F08ECIF1074 Elicited cell cult clone NF036F08EC 5', mRNA sequence.
BF645522
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/tissue_type="mixed_tissues"
/dev_stage="various_stages"
/lab_host="XLOLR"
/clone_lib="MTUS"
/note="Vector: pBluescript_SK-; Site_1: EcoRI; Site_2:
xhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap_XR vector from
Stratagene and packaged using Gigapack_III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
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VandenBosch, K., Endre, G., Silverstein, K. To
Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 6K unigene set: cDN
re-arrayed from various libraries
Unpublished (2002)
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Pa
Tel: 612 624 2755
Fax: 612 625 1738
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Pred. No. 3.6e-37;
0; Mismatches 155;
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/mol_type="mRNA"
/cultivar="A17"
                     812 bp mRNA
truncatula cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: kvandenbeccs.

Alias Clone pMHRP-28F3

TIGR sequence name: MTUCF91TV

More information is available at: ww

Seq primer: (gtA AtA CgA CtC ACt AtA

Location/Qualifiers
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                                                                           /note="Organ: root hairs; Vector: pCR2-1 Topo; Cgenerated from soybean root hair tissue treated Bradyrhizobium japonicum for 3 hours."
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1 (bases 1 to 866)
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Unpublished (2003)
Contact: Mitsuo Omura
Department of Citrus Research
National Institute of Fruit Tree Science,
Okitsu 485-6, Shimizu, Shizuoka 424-0292,
Tel: 81-543-69-7108
                                                                                                                                                                            Score 284.2; DB 14;
Pred. No. 3.8e-35;
0; Mismatches 138;
                                        hair
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root
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Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and
Expressed sequence tags from soybean root hair subtracti
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Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, N
Tel: 573-884-4752
Fax: 573-882-0588
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/mol_type="mRNA"
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Single pass sequence
Seq primer: T7.
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t; Tracheophyta; endicots;

stage

VERSION KEYWORDS

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                                                                                                     segment
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                                                                                                                             sac
                         1. .866
/organism="Citrus unshiu"
/mol_type="mRNA"
/cultivar="Miyagawa-Wase"
/db_xref="taxon:55188"
/clone="pcMFrM01.17-061"
/tissue_type="juice sac and pulp stype="juice sac and pulp stage="maturation stage"
/dev_stage="maturation stage"
/clone_lib="Citrus unshiu juice sac maturation stage"
                                                                                                                                                                          Score 283; DB 13;
Pred. No. 5.3e-35;
); Mismatches 143;
145039@affrc.go.jp.
Location/Qualifiers
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 xx145039@affrc
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71.8%;
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24-MAY-2001 7536 3',

linear EST.

cDNA clone

max

677 bp Glycine

BE823431 GM700019B20E12 Gm-r1070 mRNA sequence. BE823431

RESULT 10 BE823431/c

DEFINITION

ACCESSION

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/db xref="taxon:384""
/clone="Gm-r1070-7536"
/clone=igm-r1070-7536"
/clone lib="Gm-r1070"
/clone lib="Gm-r1070"
/note="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from immature seed coats, 3,938 from flowers, and 869 from woung pods. The 5' ESTS of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked form library Gm-r1070. The cDNA clones of the reracked form library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the month.
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                                                                                                                                                                                                                                                                    Coryell, V., Lewin, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA Tel: (217) 244-6147
Fax: (217) 233-4582
Fax: (217) 333-4582
Email: 1-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
ystems.com web site:www.genomesystems.com
Location/Qualifiers

1. .677
BEB23431.1 GI:10255665
EST.
Glycine max (soybean)
Glycine max
Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                      Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGTAAGATATGCCCCCGTCGTTCCTGTTAATGCCCCAAAGCTCGCCTGACTACATT
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                                                                                                                                                                                                                                                                                                                                                                                       Other ESTs: AW471508 corresponding to Gm-c1029-983 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., C
Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and
A Functional Genomics Program for Soybean (NSF 9872565)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewin, H. A., Director, Keck Center for Comparative and
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/mol_type="mRNA"
/db xref="taxon:3847"
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/dev stage="in vitro grown stem cuttings"
/lab_host="SOLR"
/clone lib="potato roots"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University, Tanksley lab;
sequencing; The Institute for Genomic Research. Roots were
isolated from in vitro grown stem cuttings on CM medium.
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                              799 bp mRNA linear EST 10-MAR-2003 potato roots Solanum tuberosum cDNA clone cPRO18M20 5'
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Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 799)
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.
Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,
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CCAAAATCCGAGTTTTACAAAGTAGAAGCGATTCTCAGNNCATGGCGAGTTCNNNNGGTT
                                                                                        GSTGCTCAAGGTGGTTCAACTGAGGCAGGGCGGCTCAGAATTTTCTGAAGACAAGTTT
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                             TCIGCGGCTTTGTTGAAATGGGAATTCGTGGTGTCACTGTATCTGATGTCAGGGCTTT
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This clone can be obtained from the University
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.
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/mol_type="mRNA"
/cultivar="Kennebec"
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Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
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The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:4113"
clone="cPRO18M20"
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Location/Qualifiers
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BI932336

EST55225 tomato flower, 8 mm to preanthesis buds Lycopersicon esculentum cDNA clone cTOC22H10 5' end, mRNA sequence.
BI932336.1 GI:16246808
EST.
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 711)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
Institute
Seq primer: T3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/mol_type="mRNA"
                                 155;
   Score 276; DB 12
Pred. No. 6.9e-34
; Mismatches 15!
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     30.8%;
ilarity 70.4%;
Conservative
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Unpublished (2001)
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Query Match
Best Local Similarity
watches 369; Conser
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Location/Qualifiers
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            /db_xref="taxon:4081"
/clone="cTOC22H10"
/tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/dev_stage="buds 8mm to preanthesis buds
/clone_lib="tomato flower, 8 mm to preanthesis buds
/clone_lib="tomato flower, 8 mm to preanthesis buds
/note="Vector: pBluescript SK(-); Site_l: EcoRI; Si
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flo
were taken from greenhouse plants (4-8 wks old, TA4
They were immediately frozen in liquid nitrogen and
size-separated while remaining frozen."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudico
asterids; lamiids; Lamiales; Antirrhinaceae; Antirrhineae
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AJ558383 Autirrhinum sequence.
AJ558383.1 GI:31660955
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                                                                                                                                                                                         Score 275.8; DB 12;
Pred. No. 8e-34;
; Mismatches 127;
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Zachgo, S., Stueber, K., Saedler, H.,
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Ge
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    cultivar="TA496"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Generation of ESTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
                                                                  whole
                                                                                                  Score 275; DB 9; I
Pred. No. 1.1e-33;
); Mismatches 95;
1. .732
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018 1 07 f22"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW035791
EST281945 tomato callus, 7
CLEC36D8, mRNA sequence.
AW035791
AW035791.1 GI:5894547
                                                                                                                          0;
                                                                                                  Best Local Similarity 77.8%;
Matches 332; Conservative
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361
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Best Local S
Matches 339
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                                                                            /mol_type="mkNA"
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/db_xref="taxon:4081"
/clone="clEC36D8"
/tissue_type="callus"
/dev_stage="25-40 days old"
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/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
xhol; supplier: Giovannoni laboratory; clEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648 bp mRNA linear EST 18-MAY-2001
resistant, Cornell Lycopersicon esculentum cDNA
mRNA sequence.
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Lycopersicon esculentum
Elycopersicon esculentum
Elycopersicon esculentum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 648)
D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Joton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y.,
Eliang, F., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              662
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                                       organism="Lycopersicon esculentum"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 274.2; DB 9;
Pred. No. 1.6e-33;
0; Mismatches 128;
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larity 73.3%;
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EST254179 tomato x clone cLER5E12, mR A1773079
A1773079.1 GI:527
Locat
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351; Conser
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                                                                                                                                                                                                                        /cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)
/db xref="taxon:4081"
/db xref="taxon:4081"
/clone="cleR5E12"
/dev stage="4-week old"
/dev stage="4-week old"
/dev stage="4-week old"
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; cleR - Tomato Pseudomonas Resistant EST Library.
Xho1; cleR - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript
SK(-) at 5' end with EcoRI and 3' end with XhoI site."
                                                                                                                                                                                                                             Maker)
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Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudoconas resistant tomato
Unpublished (1999)
Contact: CUGI
Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         648;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 274.2; DB; Pred. No. 1.5e-3
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                                                                                                                                                                                                 /organism="Lycopersicon
/mol_type="mRNA"
/cultivar="R11-12 (358:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGATGACAGGAGGCGATCTGACATG
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Job time : 2080.03 secs
                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 30.6%;
Local Similarity 75.7%;
nes 339; Conservative
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Search time 1738.01 Seconds
  (without alignments)
14663.718 Million cell updates/sec
                                                                                  588
                                                                                  .. GIGATAIGCTITCACCGICT
                                                                                                                                  6940544
5.1.6
Compuger Ltd.
                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                     residues
version -
                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                           model
                                                                                                                     21671516995
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                                                                    US-09-756-541-15
588
1 ATGGCGGCGTCAATGACGAA..
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                                          13:35:34
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em_ro:*
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( Dases 1 to 817)

Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.

Plant nitrogen regulatory P-PII genes

Patent: US 6177275-A 13 23-JAN-2001;

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/organism="unknown"
/mol_type="unassigned DNA"
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VSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKMEIVVKKDQVESVINTIIEGARTGEI
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                                                                                              Direct Submission
Submitted (14-MAR-2003) Salk Institute Genomic Analysis Lal
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla,
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this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/
contributed equally to this work as PIs.
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Pred. No. 4.8e-61
0; Mismatches 16
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 16 23-JAM-2001;
Location/Qualifiers
1. .594
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/organism="unknown"
/wol_type="unassigned DNA"
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 844)
Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.
A PII-like protein in Arabidopsis: putative role in nitrogen
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LVTKSPSNNSRVLPVVSAQISSDYIPDSKFYKVEAIVRPWRIQQVSS
VSDVRGFGAQGGSTERHGGSEFSEDKFVAKVKMEIVVKKDQVESVIN
GDGKIFVLPVSDVIRVRTGERGEKAEKMTGDMLSPS"
        GGCTCTGAGTTCTCGGAAGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTG
                                                                             GGTGATGGCAAGATTTTTTTTTTTGCCTGTGTCAGATGTCATAAGAGTTAGGACAG
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Proc. Natl. Acad. Sci. U.S.A. 95 (23), 13965-13970 (1998
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M. Direct Submission
Submitted (29-SEP-1998) Biology, New York University, Washington Square East, New York, NY 10003, USA Location/Qualifiers
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100.0%; Pred. No. 2.7e-137;
:ive 0; Mismatches 0;
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product="PII protein"
protein_id="AAC78333.1"
db_xref="GI:3885943"
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/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="IV"
/map="10.8 cM"
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Arabidopsis thaliana PII
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|| Similarity 70.3%; Pred. No. 4.7e-61
| 397; Conservative 0; Mismatches 16
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-F
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 14 23-JAN-2001;
Location/Qualifiers
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/mol type="unassigned DNA"
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AVKRVRYAPVVPVINAQSSPDYIPDAKFYKVBAILRPWRVSQVSSALLKIGIRGVTVS
DVRGFGAQGGSTERQGGSEFSEDKFVAKVKMEIVVSKDQVEDVIEKIIBRARTGEIGD
GKIFLLPVSDVIRVRTGERGDKARRMTGGRSDMSTSA"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
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1 (bases 1 to 840)
Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.
A PII-like protein in Arabidopsis: putative role in nitrogen
CCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAAATTGGTATTCGAGGTG1
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M.Direct Submission
Submitted (29-SEP-1998) Biology, New York University,
Washington Square East, New York, NY 10003, USA
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:3988"
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/protein_id="AAC78332.1"
/db_xref="GI:3885941"
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 Mismatches
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/mol_type="mRNA"
/db_xref="taxon:4081"
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RSNGNASVLPKIRAQNLPDYVPRSKFYKVBAILRPWRIPQVSSGLLKMGIRGVTVSDV
KGFGAQGGSKERQGGSEFSEDNFVAKVKMEIVVRKDQVBAVINKIMETARTGEIGDGK
IFLIPVSDVIRIRTGERGBQARRAGGLTDALYV"
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Submitted (22-FEB-2001) Molecular Biology FUniversity, Corner of Knox and College, Las
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protein_id="AAK16221.1"
'db_xref="GI:13277515"
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db_xref="taxon:3879"
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Score 250.8; DB 8 Pred. No. 1.9e-52;

42.78; 76.18;

Local Similarity

Query Match Best Local

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/gene="GLB1"
/note="similar to nitrogen regulatory protein PII"
/codon_start=1
/product="PII-like protein"
/protein_id="AAR14689.1"
/protein_id="AAR14689.1"
/db_xref="GI:38231570"
/translation="MASPSLSKSNFSLHSFSSPSLSQFPHFTSITVVQPKFFPSQLTFKRCQNAPSFPIIRAQNSPDFVPDAKFYKVEAILRPWRIQQVSSALLKMGIRGVTVSDVRGFGAQGGLTERQAGSBFSEDTFVAKVKMEIVVSKDQVEGVIAKIIEEARTGEIGDGVRFTTPISDVIRVRTGERGEKAERMMGGHADMSSALSTS"
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1 (bases 1 to 947)
Walch-Liu, P., Roemheld, V. and von Wiren, N.
A PII-like protein in tomato
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Canton, F.J.
Direct Submission
Submitted (11-JUN-2002) Canton F.J., Molecular Biology
Biochemistry, Faculty of Sciences, Campus de Teatinos s
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                       Indels
Length
Score 245; DB 8; 1
Pred. No. 5.4e-51;
; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPI489604 1085 bp mRNA Pinus pinaster mRNA for PII-like protein AJ489604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="putative nitrogen/codon_start=1/product="PII-like protein"/protein_id="CAD33967.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pinus pinaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="xylem"
/dev_stage="adult_tree
1. .1085
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A PII-like protein from xylem
Unpublished
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glb gene, PII-like protein.
Pinus pinaster
Pinus pinaster
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/function="-
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12. .773
ch 41.7%;
il Similarity 72.5%;
317; Conservative
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Submitted (23-MAR-1999) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724
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/db_xref="GI:37653227"
/translation="MAAHLPLFVKGSIFSLPSSTSTSSSCTYSSISHTAASPGFHSSP
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SKVKMEIVVSKDQVEAVIDAIIDEARTGEIGDGKIFVVPVADVIRVRTGERDLKPERM
AGGDQRYLQVYIKRLQTATKSLLAL"
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Direct Submission
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1 {bases 1 to 120185} Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K., Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A., Parnell, L.D., Dedhia, N.N. and McCombie, W.R. Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAT
                                                                                                                                                                                                                                                                 TGTCAGACCATGGAGAATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGG
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                                                                                                                                                                                                TAGTGCCCAAATATCTTCTGATTATATTCCAGACTCGAAATTTTACAAGGTGGAAGCAAT
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Pred. No. 4.
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Parnell, L.D.
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Arabidopsis thaliana Ecomplete sequence.
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AC007138.1 GI:4510323
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70.9%;
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Direct Submission

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COMMENT

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PFLPFLNNWLISVSRQKHQDKVLVIAEDYITLYKVNEKWPGHAVLIPPALDSKTAFSF
GSQGFFNFTARRPQHILQILBLGYNVMYNDVDMVWLQDPFLYLEGSHDAYFTDDMPQI
KPLNHSHDLPHPDRNGETYICSCMIYLRPTNGAKLLMKKWSBELQSQAWSBSIRFKAN
DQPAFNLALNKTAHQVDLYLLSQVAFPTGGLYFKNEAWVQETKGKHVIVHNNYIIGYD
RKMKRPQDYGLWLVDDHALBSPLGKLE"
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PRMLTKHIPNLAASRNVPVLYVRDNKRASLRLGBLVKLKTALAIGIKARGNDLNLLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evidence=not_experimental
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protein_id="AAD22640.1"
'db_xref="GI:4558547"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILGKVHTLLTFKVLTFLLKIELQCVFSDCVYVAETGIVVNIPTTKAQDGRPAGESGSK
LRDBYILRGLNNGLLFDKAYRVDGHGKKDWMKKDGPKLGLYGWIAGADDYNVDGREGE
ESAKLNAIQERTWRHIQKIVDDHERLTKLLESEKKKLEIKGNELAKPOVHNGTERMKL
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DIIPKDLVEKBAELADLNKFNQTLILRERRTNDELQEARKELVNCMGELVRKPFVDAM
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ADLGDGPYNAVTKALLEINEYNPSGRYITTELWNFKEDKRATLEEGVTCLLDQWEKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank accession numer
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functional catalog
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14020. .14244)
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AF104919; functional catalog
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join(10826. .10842,10929. .1
12260. .12433,12526. .12762)
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TI5B16.7, GenBank accession
                                                                     16.8, GenBank accession edited on 3 Mar 99"
                                               'note="encodes hypothetical
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| gene="T7811.3"
                                                                                                                                                                                                                      AF104919; Similar to T7B11.
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      ooo. .lUliZ
gene="T7B11.3"
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RPICRHCKSHCIPPIILKKIGTSDPYFCSLDCIBSFKRLWRAK"
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                               Cold Spring
                                                                                                     laps with
of T7B11 i
                                                                                                                                                      GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               model
     Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spr Harbor, NY 11724

Arabidopsis thaliana BAC T7B11 from chromosome IV near 9.5 cM
The T7 end of T7B11 is oriented toward the NOR and overlaps with T15B16, GenBank accession number AF104919. The SP6 end of T7B11 oriented toward the centromere and overlaps with T10M13, GenBank accession number AF001308. There are no discrepancies found in these independently finished overlaps. The region from position 110064 to 110253 exists as single stranded and single chemistry. Please see the feature below for details.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; identicanumber AF104919;
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last edited on 3 Mar 99"
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                                                                                         REMARK
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/ ULD_ALELETSFIREMED: USSILL
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             itry and other sequences of chromosomes 3, 4 at: http://www.mips.biochem.mpg.de/proj/thal/overlap with ATCHRIV4 at the 5' end and an i at the 3' end.
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.12905,12987.
.13904,13995.
of analysis and a more detailed
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                 cation of this entry and of can be viewed at: http:/s fragment has an overlap vilap with ATCHRIV6 at the Location/Qualifiers
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ich, UK,
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1 (bases 1 to 198220)

Spiegel, L.A., Huang, E.N., Nascimento, L.U., de la Bastide, M., Vil, D.M., Preston, R.R., Matero, A., Shah, R., O'Shaughnessy, A., Rodriguez, M., Shekher, M., Schutz, K., See, L.H., Swaby, I., Habermann, K., Dedhia, N.N., Mewes, H.W., Lemcke, K. and Mayer, K.F.X
  .15946,
.16885,
.18205,
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Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, B-1
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambi
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich,
E-mail: michael,bevan@bbBrc.ac.uk
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                                                                                                                                                                                                          protein
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.18989,19082.
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    15196. .15263,15359. .15510,15686. .15787,15883
16035. .16134,16215. .16361,16449. .16515,1671(
17107. .17274,17533. .17646,17718. .17831,1798
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19231. .19647)}
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.18684,18783.
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Pred. No. 8.7e-40;
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AL161493
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                                                                                                                                                                                   experimental
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EU Arabidopsis sequenc
Direct Submission
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99.0%;
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SGLVLENVKGDIELCHISFTYQTRPDVQIFRDLCFAIRAGQTVALVGESGSGKSTVIS
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ASEAEIIAAAELANAHGFISSIQQGYDTVVGERGIQLSGGQKQRVAIARAIVKRPKIL
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VLAFVKGWLLTLVMLVSIPLLAIAGAAMPIIVTRASSREQAAYAKASTVVEQTLGSIR
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SHSELLKDHEGAYAQLIRLQKIKKEPKRLESSNELRDRSINRGSSRNIRTRVHDDDSV
SVLGLLGRQENTEISREQSRNVSITRIAALNKPETTILILGTLLGAVNGTIFPIFGIL
FAKVIEAFFKPPHDMKRDSRFWSMIFVLLGVASLIVYPMHTYLFAVAGGRLIQRIRVM
CFEKVVHMEVGWFDDPENSSGTIGSRLSADAALIKTLVGDSLSLSVKNAAAAVSGLII
AFTASWKLAVIILVMIPLIGINGYLQIKFIKGFTADAKAKYEEASQVANDAVGSIRTV
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ILKKGYTGGEVVNVMVTVVASSMSLGQTTPCLTAFAAGKAAAYKMFEJ
DLNGKVLEDIRGEIELRDVCFSYPARPMEEVFGGFSLLIPSGATAALV
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/gene=*AT4g01820"
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 13835. .11101,11218.
13293. .13514,13592. .
/gene="AT4g01820"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         902 bp mRNA linear PLN 24-JUL-2003 (japonica cultivar-group) cDNA clone:J013149B08, full
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/gene="AT4g01830"
complement(join(14552. .14905,14994. .15290,15475.
15809. .16075,16311. .17110,17180. .17979,18068.
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FLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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ramamoto, m.
Falls Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ku, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, R., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Maki, K.,
Yasunishi, A. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fudachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Totta, I. Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I. Kanagawa, S., Katch, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kodayashi, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, M., Mamiki, T., Marikawa, R., Nishura, J., Nishi, K., Oka, M., Ocka, H., Sakai, K., Osato, N., Ota, Y., Otomo, M., Ohtsuki, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugani, T., Tomaru, A., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tawamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yong, Yong, Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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Shiraki, T.
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Kagawa,I.
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Itoh, M.,
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Ful
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itc
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oca, Y.
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shir
Yoshino, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                           of over 28,000 cDNA
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japonica rice
Science 301 (5631), 376-379 (2003)
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Yamamoto, M.
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,M., Suzuki,K., Li,C., Soine,K., Soine,Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Isda,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Rusosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Mixura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., Ishibiki,J., Kawamata,M., Yoshimura,A., Mura,J., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Kawai,J., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
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AK099152.1 GI:32984267
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FLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhartoideae; Oryzeae; Oryza.
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106;
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J013149B08"
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/organism="Oryza sativa (japonica cultivar-group)

Location/Qualifiers

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Vamena, E., Vamena, Manalysis Group: Otomo, Y., Iida, Y., Yamamoto, M. PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Miura, J., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, R. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Alamagaki, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Konda, M., Koyawa, H., Kondo, S., Konno, H., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Shinagawa, A., Shiraki, T., Sakai, C., Sakai, K., Sakazume, N., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Tagami, M., Tagami, Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

Isasaki, D., Satoh, W., Shibataki, Y., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.
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S ddachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Rdachi, J., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashidaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Horta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Horta, I., Iida, J., Ishikawa, M., Itoh, W., Kadawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kowamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, H., Kouda, M., Kodama, T., Kojima, Y., Kondo, J., Mivazaki, A., Matsubara, C., Kurosaki, T., Miura, J., Miyazaki, A., Matsubara, K., Murata, M., Nagata, T., Nakamura, M., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Mikura, J., Nishi, K., Nomura, K., Sakai, K., Otno, M., Ohtsuki, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Shibata, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Taya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.
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33.9%; Score 199.4; DB 8; 71.3%; Pred. No. 1.6e-39; iive 0; Mismatches 106;

Conservative

263;

Matches

Similarity

Query Match Local

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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S chmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
B 22683290
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Rest
Carl-von-Linne Weg 10, 50829 Kceln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
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/clone six weeks old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a foreceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-Not!,

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Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Seki, M., Narusaka, M., Ishida, J., Kawai, J., Itoh, M., Ishii, Y., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)

Londact: Motoaki Seki
Unpublished (2002)

Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyaɗai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060

Email: mseki@rtc.riken.go.jp
Rmail: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 566)
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AU236084 RAFL14 Arabidopsis thaliana cDNA clone RAFL14-63-K15
mRNA sequence.
AU236084
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                                               80.6%; Score 474; DB 9; I
97.8%; Pred. No. 9.9e-123;
ive 0; Mismatches 8;
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="RAFL14-63-K15"
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/lab_host="DH10B"
/clone_lib="RAFL14"
/note="Site_1: BamHI;
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669 bp mRNA linear EST 10-JUL-2003
Brassica napus cDNA clone BN25045G20, mRNA
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Brassica napus
Brassica napus
Brassica napus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 669)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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            93, rue Henri Rochefort 91025 EVRY CEDEX France.
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the free plant genomics programme 'Genoplante' (http://www.genoplante.and.http://www.genoplante.info.infobiogen.fr).
Location/Qualifiers
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larity 85.4%; Pred. No. 9.8e-114;
Conservative 0; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Brassica napus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:3708"
/clone="BN25045G20"
/tissue type="seed"
/clone_lib="BN25"
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BN25.045G20F020108 BN25 B
sequence.
CD822497
CD822497.1 GI:32504437
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AUTHORS
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COMMENT
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 685)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Genoplante.
Genoplante, a major partnership french program in
Unpublished (2003)
Contact: Genoplante
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Pred. No. 3.5e-114;
); Mismatches 82;
                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                  CD825321
BN25.060G17FC11129 BN25 Brassica napus sequence.
CD825321
CD825321.1 GI:32507261
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/organism="Brassica napus"
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/db_xref="taxon:3708"
/clone="BN25060G17"
/tissue_type="seed"
/clone_lib="BN25"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Brassica napus
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l Similarity 85.6%;
506; Conservative
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Best Local S
Matches 506
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 745)
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Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
1. .745
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                                                                                        AAG---AACATTGCTTTCTCTGATTGCATTTCGATTCTGGATTCAGACATTCCCGA
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                                                                                                                                     AAGAAAGAACAAGTGGAGTCTGTAATCAACACCATAATCGATGGAGCAAGAACAGGAGAG
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Brassica napus
Score 442.2; DB Pred. No. 1e-113; Mismatches
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Genoplante, a major partnership fr
Unpublished (2003)
Contact: Genoplante
Genoplante
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BN20.047L06F011226 BN20 B
sequence.
CD819046.1 GI:32500986
EST.
Brassica napus (rape)
Brassica napus
                       0;
Query Match
Best Local Similarity 85.4%;
Matches 505; Conservative
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Location/Qualifiers
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                   | <del>(</del>2222)
                                                                                            AAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAG
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicorosids; eurosids II; Brassicales; Brassicaceae; Brassica
1 (bases 1 to 732)
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     AAG---AACATTGCTTTCTCTGATTGCATTTCGATTTGTTCTGGATTCAGACAT
               plant
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Genoplante, a major partnership
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/clone="BN25040D05"
/tissue_type="seed"
/clone_lib="BN25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mol type="mRNA"
cultivar="Jet neuf"
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sequence.
CD820903
CD820903.1 GI:32502843
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Similarity
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cDNA clone V-B-112
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Vitis aestivalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core er
rosids; Vitaceae; Vitis.
                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 782)
Hou, H.S., Phanikanth, T.V., Kovacs, L. and Qiu, W.P. Expressed sequence tags of young leaf tissues of disease-resistant Vitis aestivalis var. Norton Unpublished (2003)
Contact: Wenping Qiu
                                                               Score 440.6; DB 14;
Pred. No. 2.8e-113;
); Mismatches 84;
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V-B-112F06 VAN-Baker-1 Vitis aestivalis
mRNA sequence.
/mol_type="mRNA"
/cultivar="Jet_neuf"
/db_xxef="taxon:3708"
/clone="BN20047206"
/tissue_type="seed"
/clone_lib="BN20"
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                                                                 74.9%;
85.3%;
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/db xref="taxon:3605"
/clone="V-B-112F06"
/tissue_type="Leaf"
/dev_stage="Young leaf"
/dev_stage="Young leaf"
/lab_host="XL10-Gold E .coli"
/clone_lib="VAN-Baker-1"
/note="Vector: pBluescript II SK (+) Phagemid; Site_1: Xho
I; Site_2: EcoR I; VAN-Baker-1 is a cDNA library of Norton
grape young leaves (Vitis. aestivalis var. Norton). Norton
grape young leaves (Vitis. aestivalis var. Norton). The cDNA synthesis and library construction was performed according to the instruction manual for pBluescript II XR
cDNA library construction kit provided by Stratagene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 782;
Southwest Missouri State University-Mountain Grove 9740 Red Spring Road, Mountain Grove, MO 65711-2999 Tel: 417 926 4105 Fax: 417 926 6646
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Pred. No. 2.8e-65;
0; Mismatches 134
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column:
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/mol_type="mRNA"
/cultivar="Norton"
                                                                                         Std Error:
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                                                                                                                                              stop:
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                                                                     Email: weq070f@smsu.edu
Insert Length: 782 Std
Plate: VAN-Baker-1-12 rc
Seq primer: T3 PRIMER
High quality sequence stc
POLYA=No.
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larity 72.7%;
Conservative (
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clone

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linear EST 12-JUL-2000
clone pMHRP-28F3, mRNA
                                                                                                          12-JUN-2003
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Eukaryota; Viridiplantae; Streptophyta; Embrycphyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Lamiales; Antirrhinaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                  Schwarz-Sommer,
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Antirrhinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_1_07_f22"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant
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Pred. No. 2.9e-60;
0; Mismatches 92;
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EST403599 MHRP- Medicago truncatula cDNA
sequence.
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AJ558383 Autirrhinum majus whole plant AJ558383 Autirrhinum majus whole plant 018 1 07 £22, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                               Zachgo, S., Stueber, K., Saedler, H.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, G
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ilarity 77.0%;
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/dev_stage="ripening Grape berries Lambda Zap II Library"
/clone lib="Ripening Grape berries Lambda Zap II; Site_1: Eco
RI; Site_2: XhoI; Oriented library, construction described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001"
      0-JUL-2002
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                                                                                                                                                                                                                                                                                             Grimplet, J
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        BQ798001
EST 6939 Ripening Grape berries Lambda Zap II L
vinifera cDNA clone RT093C02 3", mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Romieu C.
Contact: Romieu C.
Unite de Recherche des Produits de la Vigne
Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpeliier Cedex 01, 1
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embry
Spermatophyta, Magnoliophyta, eudicotyledons,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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Pred. No. 4.4e-63;
0; Mismatches 97;
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clone="RT093C02"
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/cultivar="Shiraz"
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larity 76.8%;
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Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="MHRP-"
/clone lib="MHRP-"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
Xhol; At the trifoliate stage, M. truncatula plants were
transplanted to phosphate-free sand and grown for a
further 30 days. During this period, they were fertilize
twice weekly with 1/2 Hoaglands solutions containing 20u
potassium phosphate. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into the
Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Za
                                                                                  eophyta;
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ifolieae;
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                                                                                                                                                                    Hansen,
                                                               Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embrycphyta; Trach
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Tri
Medicago.
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                                                                                                                                   Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Hanse
Holt, I.E., Cho, J. and Fraser, C.M.
ESTs from phosphate-starved roots of Medicago truncatula
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                  Email: mjharrison@noble.org
The Samuel Noble Roberts Foundation: N265417e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                    73401,
                                                                                                                                                                                                                                                                                                                                                                                      More information is available at. .
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC)
Location/Qualifiers
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Pred. No. 1.6e-58;
); Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="roots"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                  Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580-223-5810
Fax: 580-221-7380
                                                 medic)
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XLOLR cells."
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clone="pMERP-28F3"
                                                                                                                                                                                                                                                                                                                                                                         TIGR sequence name: MTHAC26TK
                                                  (barrel
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                  GI:9055733
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|larity 75.6%;
|Conservative (
                                                truncatula
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Plant Biology Div
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306; Conser
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EST.
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/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:

xhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction, cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
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                                          526
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.

ESTS from developing reproductive tissues of Medicago truncatula Unpublished (2001)

Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITIACCIGICGILIAGIGCCCAAAIAICITCIGAITATATICCAGACICGAAAITITACA
                                        GGACAGGAGATTGGTGATGCCAAGATTTTTGTTTTGCCTGTGTCAGATGTCATAAGAG
                                                                   GAACTGGGGAGATTGGTGATGGCAAATTTTCTTGATCCCTGTATCTGATGTAATAAGAA
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413 AAATAGTGGTGAAAAAAACACCAGGTTGAGGCAGTGATAAACAAAATTATGGAGACGGCAA
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                                                                                                                                                                                                                                                                                         714 bp mRNA linear BST GESD Medicago truncatula cDNA clone pGESD9J4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at: www.medicago.org
gtg gAT CC).
                                                                                                                                527 TTAGGACAGGTGAGCGTGGGGAGAAAGCAGAGAAGATGACTGGTG 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="A17"
/db_xref="taxon:3880"
/clone="pGESD9J4"
/tissue_type="immature seeds"
/dev_stage="Immature seeds, 11 to
                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR sequence name: MTPAP50TK
More information is available
Seg primer: SKmod (CTA gAA CTA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lib="GESD"
                                                                                                                                                                                                                                                                                                                                                                               GI:14985399
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XLOLR cells."
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BI311072.1 GI:
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mRNA seguen
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/db_xref="taxon:4081"
/clone="clEC36D8"
/tissue_type="callus"
/dev_stage="25-40 days old"
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EST281945 tomato callus,
CLEC36D8, mRNA sequence.
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                                                                  41.9%;
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AUTHORS
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LOCUS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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231
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                                                                                                                                                                                                                                                                          GAACTGGGGAGATTGGTGATGGCAAATTTTCTTGATCCCTGTATCTGATGTAATAAGAA
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                                                                                 TCGGGATTCGAGGTGTTACTGTTTCTGATGTGAGGGTTTGGTGCACAAGGAGGTTCTA
                                                                                                 AAATCGTTGTTAAGAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAA
TTCTTCCCAAAATCAGAGCTCAAAACCTTCCTGACTAGGTTCCTGAATCCAAGTTTTACA
                                                      AAGTIGAAGCCATTCTCAGGCCATGGAGAATCCCTCAGGTTTCTTCGGGTTTGTTGAAAA
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The Medicago truncatula 6K unigene set: cDNA clones selere-arrayed from various libraries
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clone MTUS-58H7
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/mol_type="mRNA"
/cultivar="A17"
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/tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_host="XLOLR"
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MTUS Medicago truncatula
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CtC ACt A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR sequence name: MTUCF91TV
More information is available
Seq primer: (gtA AtA CgA CtC A
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kvandenb@cbs.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lib="MTUS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:27409759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: kvandenb@cbs.um
Alias Clone pMHRP-28F3
TIGR sequence
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linear EST 18-MAY-2001 esculentum cDNA clone
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Lycopersicon esculentum
Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 613)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATCGTTGTTAAGAAAGACCAAGTGGAATCTGTAATCAACACAATAATTGAAGGAGCAA
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extracts. Plasmids containing cDNA inserts were excision the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                            812;
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Clemson University Genomics Institute
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
5 prime sequence.
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Generation of BSTs from tomato callus tissue
Unpublished (1999)
Contact: CUGI
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TAMU Lycopersicon
                                                                                                            DB 14;
                                                                                                           Score 246.6; DB 14;
Pred. No. 1.7e-58;
; Mismatches 99;
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'mol_type="mRNA"
'cultivar="TA496"
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er, C.M.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycoper;

1 (bases 1 to 702)

van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsi

Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Frase;

Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.

Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA linear EST 18 preanthesis buds Lycopers 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Gen
                                                                                                                                                                      GGTCACAAAGTCACCGAGTAATAACAGTCGTGTTTTACCTGTCGTTAGTGCCCAAA
                                                                                                                                                                                                                    TICTGATTATATICCAGACTCGAAATTTTACAAGGTGGAAGCAATTGTCAGACCAT
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                                                                                                                                                                                                                                                                    AATCCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGGTGTTACTGTT
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                                                                                                                       613;
                                                                                                                                               Indels
                                                                                                                         Length
                                                                                                                                    -58;
120;
                                                                                                                       Score 245; DB 9;
Pred. No. 4.4e-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Email: http://www.genome.clemson.edu/c
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 702 bp clower, 8 mm to clone cTCC22G23
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                                                                                                                       41.7%;
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EST552012 tomato 1
esculentum cDNA c3
BI932123
BI932123.1 GI:163
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Best Local Similarity
Matches 317; Conser
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AUTHORS
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/mol type="mRNA"
/cultivar="TA496"
/db xref="taxon:4081"
/clone="cTOC22G23"
/tissue type="flower"
/dev stage="buds 8mm to preanthesis"
/clone lib="tomato flower, 8 mm to preanthesis buds"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 711)

van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,

van der Hoeven, R.S., Ronning, C.M., Nierman, W., Fraser, C.M.,
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BI932336.1 GI:16246808
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                                                                  organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 245; DB 12;
Pred. No. 4.6e-58;
0; Mismatches 120;
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          Location/Qualifiers
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|larity 72.5%;
|Conservative
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Best Local Similarity
Matches 317; Conser
Seq primer
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F. F.

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/organism="Lycopersicon esculentum"
/organism="Lycopersicon esculentum"
/collivar="TA496"
/clone="cTOC22H10"
/tissue_type="flower"
/tissue_type="flower"
/tissue_type="flower"
/clone lib="tomato flower, 8 mm to preanthesis buds"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
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Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
preanthesis
Unpublished (2001)
Contact: CUGI
Contact: CUGI
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Gen
Institute
Seq primer: T3.
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ATGGCGCCGTCAATGACGAA.... Sequence:

588

.....GTGATATGCTTTCACCGTCT

Gapext 1.0 IDENTITY NUC Gapop 10.0, Scoring table:

residues 2124099041 seds, 3373863 Searched: 6747726 hits satisfying chosen parameters 벟 Total number

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Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databas

Geneseq 29Jan04:\*
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geneseqn2003s:\*
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## SUMMARIES

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## ALIGNMENTS

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Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening; ss.
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Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters. Claim 2; Col 37-38; 35pp; English. 2001-158572/16 WPI; 2001-158572 P-PSDB; AAB69495 useful Novel

clones The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clowith the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants S

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                                                                                                                          The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: {a} contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and {b} detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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165;
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                                                                             Score 285; DB 4
Pred. No. 4.1e-7
; Mismatches 1
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(Methanococcus jannaschii
Accession Aav21209
                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated Acinetobacter baumannii nucleic acids The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                               and drug
                                                                                                                                                                                                                                                               The present invention relates to a Moraxella catarrhalis genomic comprising of a combination of 41 nucleic acid molecules (see AAE AAE28554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therecompositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bactilora of human upper airways. M. catarrhalis is known to cause acilocalised infections such as otitis media, sinusitis and bronchop infection and life-threatening, systemic diseases including endocinfection and life-threatening, systemic diseases
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                                                                                                                                                                                Genomic library for identifying diagnostic and therapeutic and for identifying virulence factors, regulatory elements targets, comprises Moraxella catarrhalis nucleic acids.
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Pred. No. 8.8e-17;
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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the geneme of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P.
                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of Photorhabdus luminescens and encoded polypeptides, e.g. as therapeutic antimicrobials and agricultural pesticides.
GAGAGGGTTTGGTGCACAAGGAGGTTCTACCGAGAGACACGGTGGCTCTGAGTTCTCGGA
                                                                                               TAAGGGTAGGGGAGTTCAAGGTGGAATAGTTGAGAGGTATAGGGGGGAGAGAGTATTGT
                                                                                                                                         -TTAATTCCAAAGGTTAAGATTGAGTTGGTTGTAAAAGAGGAAGATGTTGATAA
                                                                                                                                                                                CCAGCAAGTTTCATCGGCTTTACTGAAAATCGGGATTCGAGGTGTTACTGTTTCTGATGT
                                                                                                                   AGACAAATTTGTTGCTAAAGTTAAGATGGAAATCGTTGTTAAGAAGACCAAGTGGAATC
                                                                                                                                                       TGTAATCAACACAATAATTGAAGGAGCAAGGACAGGAGAGATTGGTGATGGCAAGATTTT
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   luminescens. Cells transformed to express the genes are useful for recombinant production of the process, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides genes, proteins, vectors containing the genes and Ab are also use therapeutically (to treat microbial infection by bacteria or fung are sensitive to P. luminescens-encoded toxins or antibiotics) and biopesticides. Other uses of the genes and the proteins are as vifactors and for identifying targets of human diseases for which P luminescens is a model (particularly plague and whooping cough). Sequence represents one of the isolated P. luminescens genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins are antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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provide an opportunity to identify secreted or surface exposed proteins
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none have successfully overcome
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Corizzi,G.M., Lam,H.-M. and Hsieh,M.-H
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Hsieh,M.H., Lam,H.M., van de Loo,F.J. and Coruzzi,G.
A PII-like protein in Arabidopsis: putative role in nitrogen
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Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.M. Direct Submission
Submitted (29-SEP-1998) Biology, New York University, Washington Square East, New York, NY 10003, USA Location/Qualifiers
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       Garcia-Ibilcieta, D. and Sengupta-Gopalan, Garcia-Ibilcieta, D. and Sengupta-Gopalan, Direct Submission
Submitted (22-FEB-2001) Molecular Biology
University, Corner of Knox and College, La
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Pred. No. 2.8e-72;
0; Mismatches 153;
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/gene="GLNB"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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Pred. No. 2.5e-153;
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sativa PII protein (GLNB)
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                       /codon_start=2
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/db_xref="GI:3885941"
 ="putative
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/function="p
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Arabidopsis thaliana (thale cress)
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 591)
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Brassicaceae;
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/organism="Arabidopsis thaliana"
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Pred. No. 4.5e-68
); Mismatches 16
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Brassicales;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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165;
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Pred. No. 4.5e-68;
; Mismatches 16
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Coruzzi,G.M., Lam,H.-M. and Hsieh,M.-H.
Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 15 23-JAN-2001;
Location/Qualifiers
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                                                                                                                                                               /organism="unknown"
/wol_type="unassigned DNA
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Sequence 21
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                                                                                                                  CAAAGCTCGCCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGG
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Pred. No. 4.7e-68;
); Mismatches 165;
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Plant nitrogen regulatory P-PII genes
Patent: US 6177275-A 13 23-JAN-2001;
Location/Qualifiers
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/mol_type="unassigned DNA"
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VSDVRGFGAQGGSTERHGGSEFSEDKFVAKVYMEIVVKKDQVESVINTIIEGARTGEI
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Seki,M.,
                                                                                                                                                                                           Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,
Chan, M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
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                                                                                                 ada, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKBN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J. Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim,C.J. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
Location/Qualifiers
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Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, I
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Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M.,
Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamac
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (14-MAR-2003) Salk Institute Genomic Analysis La
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 591;
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Pred. No. 4.5e-68;
); Mismatches 165;
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'note="This clone is in pUNI
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product="At4g01900"
protein_id="AA063273.1"
db_xref="GI:28950699"
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/mol_type="mRNA"
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'db xref="taxon:3702"
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clone="U23463"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

| (bases 1 to 947)
| Walch-Liu, P., Roemheld, V. and von Wiren, N.
| A PII-like protein in tomato
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  Mismatches
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/mol_type="mRNA"
/db_xref="taxon:4081"
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/note="LeGLB1
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/product="AAC7833.1"
/protein_id="AAC7833.1"
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/translation="MAASMTKPISITSLGFYSDRKNIAFSDCISICSGFRHSRPSCLD
LVTKSPSNNSRVLPVVSAQISSDYIPDSKFYKVEAIVRPWRIQQVSSALLKIGIRGVT
VSDVRGFGAQGGSTERHGGSBFSEDKFVAKVKMEIVVKKDQVESVINTIIBGARTGEI
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trached
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
1 (bases 1 to 844)
Hsieh, M.H., Lam, H.M., van de Loo, F.J. and Coruzzi, G.
A PII-like protein in Arabidopsis: putative role in nitroges
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, USA
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Pred. No. 4.7e-68
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Hsieh, M.H., Lam, H.M., van de Loo, F.J.
Direct Submission
Submitted (29-SEP-1998) Biology, New Nashington Square East, New York, NY 1
Location/Qualifiers
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/function="putative role
/note="GLB1"
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/organism="Arabidopsis E
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/db_xref="taxon:3702"
/chromosome="IV"
/map="10.8 cM"
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                                    /product="PII-like protein"
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Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Seguencing & Analysis Group:, Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Pred. No. 2.5e-65;
); Mismatches 108;
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AUTHORS
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hayashida, K., Hayashizaki, Y., Iida, Y., Ishikawa, M., Itoh, M., Kagawa, T., Horta, I., Iida, J., Iida, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katok, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Katok, H., Koyima, K., Kojima, K., Kojima, K., Kojima, K., Kojima, T., Kodo, H., Kouda, M., Kodawa, T., Kojima, K., Murata, M., Miura, J., Miyazaki, A., Masuda, H., Matsubara, C., Kurosaki, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, C., Sakai, T., Salio, H., Sakai, T., Salio, H., Sakai, T., Salio, K., Salio, K., Shibata, K., Shinagawa, A., Shiraki, T., Salio, K., Saloh, K., Shibata, K., Shinagawa, A., Shiraki, T., Salio, M., Tagami, T., Tagami, T., Tagama, T., Tawamato, R., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
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Yamamoto, T.
Yukeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.
Yodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Nizuno, K., Narikawa, R., Niikura, J., Oka, M., Kie, Q., Yokomizo, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Kishikawa-Hirozane, T., Motsuyama, T., Miyazaki, A., Murata, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Osato, N.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Toya, T., Waki, K.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-270, 2000-201
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (B-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M.
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Fals Genome Sequencing & Analysis Group: Otomo,Y., Lida,Y., Fals Genome Sequencing & Analysis Group: Otomo,Y., Lida,Y., Fuls Genome Sequencing & Analysis Group: Otomo,Y., Lida,Y., Kobayashi,M., Kodama,T., Kuromedi,T., Lu,M., Masuda,H., Miura,J., Nizuno,K., Narikawa,R., Mikura,J., Oka,M., Kyu,R., Sugano,S., Sugiyama,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Immura,K., Imotani,K., Ishii,Y., Itoh,W., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kouda,M., Kishikawa-Hirozane,T., Momura,K., Muyazaki,J., Murata,M., Nishi,K., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Sahazume,N., Tagami,A., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshimura, A.

Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mail: 8kikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.
Chneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.
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/mol_type="mRNA"
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larity 70.9%; Pred, No. 6.3
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           REFERENCE
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Agrobiological Sciences Rice Full-Length cDNA Project Team:,
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Obtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yoshimura, A., Mikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mikura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y., Shibata, K., Shinagawa, A., Shiraki, T.,
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Yoshino, M., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
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FLI_CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracht Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ebrhartoideae; Oryzeae;
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                  _xref="taxon:39947
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.l Similarity 70.9%;
287; Conservative
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RTGEKNTEAV"
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                                                         CCTGACTACATTCCTGATGCTAAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGA
              CAGATTATGTCCCAGAAGCCAACTTTTACAAAGTAGAAGCAATATTGAGGCCATGGCGC
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Davis, CA 95616,
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/db_xref="taxon:63737"
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Hanson, T.E. and Meeks, J.C.
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Submitted (05-AUG-1997) Section
California, One Shields Avenue
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/function="putative r
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/trans1_table=11
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GCGAGTCTCGCAAGTTTCCTCGGCTTTGCTAAAATTGGTATTCGAGGTGTTACTGTTTC
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function="putative nitrogen sensor protein"
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Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
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Pred. No. 1e-48;
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Direct Submission
Submitted (11-JUN-2002) Canton F.J.
Biochemistry, Faculty of Sciences,
SPAIN
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'mol_type="mRNA"
'db_xref="taxon:71647"
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PII-like
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A PII-like protein from xylem
Unpublished
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dev_stage="adult tr
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Similarity 73.2%;
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| function="signaling protein"
| codon start=1
| /transl_table=11
| product="PII protein"
| protein id="CAB75358.1"
| db_xref="GOA:Q9L422"
| db_xref="GOA:Q9L422"
| db_xref="SPTREMBL:Q9L422"
| /translation="MKKVEAIIRPFKLDEVKIALVNAGIVGMTVSEVRGFGRQXGOTE
| ranslation="MKKVEIVVEDNQVDMVVDKIIAAARTGEIGDGKIFISPVEQVIRI
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                             Gaps
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Submitted (14-DEC-1999) Zhang C.C., Laboratoire de Chimie
Bacterienne, C.N.R.S., 31, chemin Joseph Aiguier, 13402 M
cedex 20, FRANCE
                                                         214 AAATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCT
                                                                          TTGCTAAAAATTGGTATTCGAGGTGTTACTGTTTCTGATGTTCGAGGTTTTGGTG
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signal transduction protein PII by
the cyanobacterium Anabaena sp. st
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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Pred. No. 1.3e-18;
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ginB gene; PII protein.
Nostoc sp. PCC 7120 (Anabaena sp. PCC
Nostoc sp. PCC 7120
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/mol_type="genomic DNA"
/strain="PCC 7120"
/db_xref="taxon:103690"
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ilarity 60.4%;
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                                 ATTCTACAAAGTGGAAGCAATTCTCAGGCCCTGGCGAGTCTCGCAAGTTTCCTCGGCTTT
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CGGCACGAGGCTACTGCGAA. US-09-756-541-16 594 1 CGGCACGAGGCTAC score: Sequence:

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. CTGACATGAGTACTTCTGCT

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residues 2124099041 3373863 seqs, Searched:

6747726 hits satisfying chosen parameters: 44 Total number

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summaries

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inted, No. is the number of results predicted by chance to have a greater than or equal to the score of the result being prime derived by analysis of the total score distribution. Pred. No. is the number of rest score greater than or equal to and is derived by analysis of

## SUMMARIES

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## ALIGNMENTS

Castor bean; PII; plant mitrogen regulatory gene; P-PII; nitrogen assimilation; transgenic plant; herbicide screening; SS. Ricinus communis P-PII cDNA fragment. BP 97US-00899330. 96US-0022328P. (UNNY ) UNIV NEW YORK STATE. entry) standard; cDNA; (first communia. US6177275-B1 23-JUL-1997; 24-JUL-1996; 23-APR-2001 23-JAN-2001 AAF 58584; AAF58584 Ricinus RESULT 1 AAF58584 

Hsieh M; WPI; 2001-158572/16 P-PSDB; AAB69496. Lam H, Coruzzi GM,

Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.

English. Col 37-38; 35pp; Claim 2; The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants

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transgenic plant; herbicide screening
           Length 594
 0 Other;
                       Indels
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           Score 594; DB 4; 1
Pred. No. 2.1e-168;
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 117 C; 157
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           Query Match
Best Local Similarity 100.0%;
Matches 594; Conservative 0;
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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clones with the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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Novel P-PII genes capable of regulating plant nitrogen assimilation, useful for transgenic plant production, and as probes for isolating additional genomic clones having P-PII gene promoters.
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Pred. No. 2.5e-168;
; Mismatches 0;
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WO200216655-A2
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                                                                                                                                                                                                                                                                                                           The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clowith the promoters of P-PII genes. P-PII promoters are light- and/or sucrose-inducible, and are suitable for genetic engineering of plants
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                                         Arabidopsis thaliana; PII; plant nitrogen regulatory gene; P-I
nitrogen assimilation; transgenic plant; herbicide screening;
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Pred. No. 2.5e-75;
); Mismatches 169
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(1 Similarity 70.3%;
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                                                                      Arabidopsis thaliana
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cress regulated gene (ABZ12196-ABZ17574) used
Note: The sequence data for this patent is
ed specification but is based on sequence
ent by the European Patent Office
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Mismatches
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SYNGENTA PARTICIPATIONS
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larity 70.3%;
Conservative (
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26-JAN-2001; 2001US-0264647P
22-JUN-2001; 2001US-0300111P
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19
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           ATTGCTTTCTCTGATTGCATTTCGATTTCTGGATTCAGACATTCCCGACCAT
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The present sequence encodes a nitrogen regulatory PII protein. Novel plant PII (also called P-PII) nucleotide sequences have been isolated. They are useful for regulating nitrogen assimilation in plants, and in transgenic plant production. They are also used to engineer organisms that overexpress wild-type or mutant P-PII regulatory proteins. P-PII proteins are useful for in vitro screening of herbicides. P-PII nucleotides may be used as probes for isolating additional genomic clor nucleotides may be used as probes for isolating additional genomic clor sucrose-inducible, and are suitable for genetic engineering of plants
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AATGGTATCACCGTCACTGAAGTCAAAGGCTTTGGTCGCCAAAAAGGTCATACCGAGATG
                          CASSGCGGCTCAGAATTTTCTGAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTG
                                                       TATCGTGGGGCGGAATATGTGGTTGAT---TTTTTACCAAAATTAAAATTGAGATAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                            sequence of Photorhabdus luminescens and encoded polypeptides e.g. as therapeutic antimicrobials and agricultural pesticides
                                            CGAGGTGTTACTGTTTCTGATGTTCGAGGTTTTTGGTGCTCAAGGTGGTTCAACTGAGAGG
                                                                          CAAGGGATTACCGTAACTGAAGTTAAAGGTTTTTGGTCGTCACAAAGGACATACAGAACTT
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              recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. Genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that e sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virula factors and for identifying targets of human diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens genes
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                              The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81260 to AAA812563 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of AAA81304 to AAA81321 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all invention. The nucleic acid invention of them, can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccines
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roteins
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                                                                                                                                                                                                                                                                                                                                                        antigen; vaccine, diagnosis; infection; antibacterial; identification; Meningococcus B; Menb, ds.
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CAAGAACTGGAGAGATTGGAGACGGCAAGATTTTTCTTGCTGCCTGTTTCAGATGTAATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis MenB polynucleotide ORF sequences, which a used in the exemplification of the present invention. The nucleic sequences, protein sequences, and antibodies against them, can be the manufacture of a composition. The composition can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     some of the identified proteins could be components of Meningococcus B; against all serotypes; and/or against and of Neissariae. Identification of sequences from the bact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing infection due to Neisserial bacteria. F
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that may be presumed targets for the immune system and antigenically variable or at least more conserved than variable regions
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Matches 184; Conservative
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	RESULT 1	
•	T15252	AMONG
	DEFINITION	crs852 lambdaZAPST Ricinus communis cDNA clone pers852 similar to
<del>:</del>		nitrogen-regulatory protein, mRNA sequence.
	ACCESSION	T15252
	VERSION	T15252.1 GI:14190796
	KEYWORDS	EST.
	SOURCE	Ricinus communis (castor bean)
10.	ORGANISM	Ricinus communis
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
		rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
		Acalypheae; Ricinus.
· · ·	REFERENCE	1 (bases 1 to 542)
	AUTHORS	vandeLoo, F.J., Turner, S. and Somerville, C.
	TITLE	Expressed sequence tags from developing castor seeds
	JOURNAL	Plant Physiol. 108, 1141-1150 (1995)
	COMMENT	Contact: Somerville CR
		Carnegie Institution
		Carnegie Institution, 290 Panama St, Stanford, CA 94305
		3251521
		Email: crs@andrew.stanford.edu
		Seq primer: T3.
	FEATURES	Location/Qualifiers
	source	1542
_		/organism="Ricinus communis"

ALIGNMENTS

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 782)
                                                                                                                                                                                                                                                                                     9
                                                   /note="Vector: lambdaZAFII; Site 1: EcoR1; Site 2: XhoI, Poly(A) + RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. CDNA was synthesized and cloned into lambdaZAPII accord: to the instructions of the manufacturer (Stratagene): synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In directionally into AhoI (3') and EcoRI (5') sites. In scases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate. "
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Hou, H.S., Phanikanth, T.V., Kovacs, L. and Qiu, W.P.
Expressed sequence tags of young leaf tissues of
disease-resistant Vitis aestivalis var. Norton
Unpublished (2003)
                                                                                                                                                                                                        Score 408.8; DB 14;
Pred. No. 9.4e-103;
1; Mismatches 18;
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/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrs852"
/clone_lib="lambdaZAPST"
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                                                                                                                                                                                                        68.8%;
illarity 95.5%;
Conservative (
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Vitis aestivalis
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CB289081
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/tissue_type="Leaf"
/dev_stage="Young leaf"
/dev_stage="Young leaf"
/lab_host="XL10-Gold E .coli"
/clone_lib="VAN-Baker-1"
/note="Vector: pBluescript II SK (+) Phagemid; Site_1: Xho
I; Site_2: EcoR I; VAN-Baker-1 is a cDNA library of Norton
grape young leaves (Vitis. aestivalis var. Norton). Norton
grape young leaves (Vitis. aestivalis var. Norton) grapevines were grown under normal greenhouse conditions.
The cDNA synthesis and library construction was performed according to the instruction manual for pBluescript II XR cDNA library construction kit provided by Stratagene."
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Department of Fruit Science
Southwest Missouri State University-Mountain Grove
9740 Red Spring Road, Mountain Grove, MO 65711-2999,
Tel: 417 926 4105
Fax: 417 926 6646
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Pred. No. 2.8e-78;
); Mismatches 130;
                                                                                                                                                90
                                                                                                                            Std Error: 0.00 row: F column:
                                                                                                                                                                                                                                                                           /organism="Vitis aestivalis"
                                                                                    Email: weq070f@smsu.edu
Insert Length: 782 Std Error:
Plate: VAN-Baker-1-12 row: F c
Seq primer: T3 PRIMER
High quality sequence stop: 782
POLYA=No.
                                                                                                                                                                                        782
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/clone="V-B-112F06"
/tissue_type="Leaf"
                                                                                                                                                                                                                                Location/Qualifiers
1. .782
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cultivar="Norton"
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llarity 75.4%;
Conservative
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Best Local Similarity
Matches 399; Conser
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RESULT

Contact: Wenping Qiu

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Pred. No. 4.6e-72;
); Mismatches 154;
                                                                                                                                                                                                 597 bp mRNA
truncatula cDNA
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/mol_type="mRNA"
/cultivar="A17"
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Tel: 580-223-5810
Fax: 580-221-7380
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'clone="pMHRP-28F3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="roots"
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                                                                                                                                                                                                BE239550
EST403599 MHRRP- Medicago
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71.8%;
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Best Local Similarity 71.8
Watches 407; Conservative
                                                                                                                             236
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BE239550.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="ripening stage"
/clone_lib="Ripening Grape berries Lambda Zap II Library"
/note="Organ: Fruit; Vector: Lambda Zap II; Site_1: Eco
RI; Site_2: XhoI; Oriented library, construction_described
in Generation of ESTs from grape Berry (skin, pulp or
seeds) at various developmental stages by Terrier, N.,
Ageorges, A., Abbal, P., Romieu, C. in J. Plant Physiol. 158
(12): 1575-83 2001."
                                                                                                                             Tracheophyta;
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Grimplet, J
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                               13
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                                                                                                      Vitis vinifera

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracl
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicor
rosids; Vitaceae; Vitis.

1 (bases 1 to 723)
Abbal, P., Agasse, A., Ageorges, A., Atanassova, R., Barrieu,
Couture, C., Dedaldechamp, F., Delrot, S., Glissant, D., Grim
Hamdi, S., Romieu, C. and Terrier, N.
Generation of Expressed Sequence Tag from Grape Berry (sk
or seeds) at Various Developmental Stages
               linear EST 3
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Institut National de la Recherche Agronomique
2, place Viala, 34 060 Montpellier Cedex 01, France
Tel: 00-33-(0)4-99-61-28-62
Fax: 00-33-(0)4-99-61-28-57
Email: romieu@ensam.inra.fr
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            Ripening Grape berries Lambda Zap II I cDNA clone RT093C02 3', mRNA sequence.
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Pred. No. 1.1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Vitis vinifera
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/clone="RT093C02"
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                    GI:22012967
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ilarity 76.0%;
Conservative
                                                                                                                                                                                                                                                hed (2002)
Romieu C.
           BQ798001
EST 6939 Ripeni
vinifera cDNA c
BQ798001
BQ798001.1 GI:
EST.
Vitis vinifera
                                                                                                                                                                                                                                                   Unpublished
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AUTHORS
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/dev_stage="phosphate-starved"
/dev_stage="phosphate-starved"
/lab_host="XLOLR"
/clone lib="MHRP-"
/clone lib="MHRP-"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; At the trifoliate stage, M. truncatula plants were
transplanted to phosphate-free sand and grown for a
further 30 days. During this period, they were fertilized
twice weekly with 1/2 Hoaglands solutions containing 20uM
potassium phosphate. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into the
Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propagated in
XLOLR cells."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
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                                                         GTCCGCACTGGTGAGGGGGGTGATAAGGCTGAGATGACAGGAGGAGGGCGATCTGACATG
                                                                                        Harrison, M.J., Town, C.D., Bowman, C.L., Craven, M.B., Harsen, T.S. Holt, I.B., Cho, J. and Fraser, C.M.

ESTs from phosphate-starved roots of Medicago truncatula Unpublished (2000)

Contact: Maria J. Harrison
Plant Biology Division

The Samuel Roberts Noble Foundation
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TIGR sequence name:MTHAC26TK
More information is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gCg gAT CC).
Location/Qualifiers
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/clone="pgESD9J4"
/tissue_type="immature seeds"
/dev stage="Immature seeds"
/dev stage="Immature seeds"
/dev stage="Immature seeds, 11 to 19 days after
pollination"
/clone_lib="GESD"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA+
enriched RNA. The cDNA was directionally ligated into
the Unizap XR vector from Stratagene and packaged using
Gigapack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propogated in
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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ESTs from developing reproductive tissues of Medicago tr
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USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
                                                                         TTTTCAAGCTTCAGCGTCATTCGCAAGCGTTTCGGAGATTC
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More information is available
Seq primer: SKmod (CTA gAA CTA
Location/Qualifiers
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Tel: 713-798-7044
Fax: 713-798-7078
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XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNI
was directionally ligated into the Unizap XR vector from
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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Medicago truncatula (barrel medic.)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicote
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VanderBosch, K., Endre, G., Silverstein, K, Town, C.D.,
Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 6K unigene set: cDNA clones
re-arrayed from various libraries
Unpublished (2002)
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Pred. No. 1.3e-71;
0; Mismatches 155;
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/mol_type="mRNA"
/cultivar="Al7"
                                                                                                                                                                                                                   Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="MTUS-58H7"
/tissue_type="mixed tissues
/dev_stage="various stages"
/lab_host="XLOLR"
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                                                                                                                                                                                                                                                                                                                     Alias Clone pMHRP-28F3
TIGR sequence name: MTUCF91TV
More information is available at:
Seq primer: (gtA AtA CgA CtC ACt
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             kvandenb@cbs.umr.edu
                GI:27409759
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/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/clone_lib="Elicited cell culture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 and
24 hours after induction. Equal amounts of RNA from each
time point were pooled and used for mRNA isolation."
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J. Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Center for Medicago Genomics Research Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF036F08EC1F1074 Elicited cell culture Medicago truncatula cDNA clone NF036F08EC 5', mRNA sequence.

BF645522
BF645522.1 GI:11910651
EST.
                                          GAAGACAATTTTGTTGCCAAAGTTAAAATGGAAATAGTGGTGAGAAAAGACCCAGGTTGAG
GAAGACAAGTTTGTTGCTAAAGTTAAGATGGAGATCGTGGTTAGCAAAGACCAGGTTGAG
                                                                                                                    GATGTTATAGAAAAATCATTGAGGAGGCAAGAACTGGAGAGATTGGAGAGGCGGCAAGATT
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Pred. No. 1.7e-70;
); Mismatches 159;
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/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF036F08EC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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Insert Length: 612 Std Error: 0.00
Plate: 036 row: F column: 08
Seq primer: TCACACAGGAAACAGCTATGAC.
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Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (barrel medic)
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/note="Organ: root hairs; Vector: pCR2-1
generated from soybean root hair tissue 1
Bradyrhizobium japonicum for 3 hours."
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                                                                DB 14;
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les 124;
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Clemson University Genomics Institute
                                                               Score 276.6; I
Pred. No. 6.3e-
0; Mismatches
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Scheffler, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and
Expressed sequence tags from scybean root hair subtractiv
                                                                                                                                                                    GITTITGATTICAGITIGITITGICCAGAGCITAGACAITCICGGITTICICACI
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subtracted
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/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Gary Stacey
University of Missouri
108 Waters Hall, Columbia, MO 65211, US
Tel: 573-884-4752
Fax: 573-882-0588
Email: staceyg@missouri.edu
Single pass sequence
Seq primer: T7.
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mRNA linear EST 18-OCT-2001 preanthesis buds Lycopersicon 5' end, mRNA sequence.
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Fraser,C.M.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 711)

van der Hoeven, R. S., Bezzerides, J. L., Karamycheva, S. A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C. M., Nierman, W., Fraser, C. M.

Martin, G. B.; Giovannoni, J. J. and Tanksley, S. D.

Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University
100 Jordan Hall, Clemson, SC 29634, USA.
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Lamiales; Antirrhinaceae; Antirrhineae;
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                                            /tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to preanthesis buds"
/clone_lib="tomato flower, 8 mm to preanthesis buds'
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site
KhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowere taken from greenhouse plants (4-8 wks old, TA4:
They were immediately frozen in liquid nitrogen and size-separated while remaining frozen."
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AJ558383 Antirrhinum majus whole plant Antirrhinum majus 018 1 07 f22, mRNA sequence.
AJ558383
AJ558383.1 GI:31660955
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                                                                                                                                                                                     Score 275.2; DB 12;
Pred. No. 1.5e-65;
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                        db_xref="taxon:4081"
clone="cTOC22H10"
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Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
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Antirrhinum BST collection
Unpublished (2003)
mol_type="mRNA"
cultivar="TA496"
                                                                                                                                                                                                                          0
                                                                                                                                                                                                46.3%;
llarity 75.9%;
Conservative
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 648)
D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y.,
Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1773079

EST254179 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLER5E12, mRNA sequence.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                            732;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                            Length
                                                                                                                                                                  whole
                                                                                                                                                                                                                            Score 275; DB 9; Pred. No. 1.7e-65; 0; Mismatches 95;
                                                      /organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_1 07_f22"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus w
  Germany
Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
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larity 77.8%;
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A1773079.1 GI:53
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 613)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T.,
Holt, I.E., Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ahn, S.,
Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and
Giovannoni, J.
                                                                                                                                                                                                                                                                                          194
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                                                                ey Maker)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 bp mRNA linear EST 18-MAY-2 TAMU Lycopersicon esculentum cDNA clone
                                                                                                /tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/clone_lib="tomato resistant, Cornell"
/rote="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_Xhol; cLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with Xhol site.
                                                                                                                                                                                                                                                                                                                                                                                                                      GGATGT
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                                                              (35S::Pto in Rio Grande x Mon
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                                     esculentum
                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                    Score 274.2; DB 9;
Pred. No. 2.9e-65;
0; Mismatches 109;
                                /organism="Lycopersicon e
/mol_type="mRNA"
/cultivar="R11-12 (355::P
/db_xref="taxon:4081"
/clone="cLER5E12"
/tissue_type="leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628
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           Location/Qualifiers
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EST281945 tomato callus, T
cLEC36D8, mRNA sequence.
AW035791
AW035791.1 GI:5894547
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339; Conser
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Matches
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AUTHORS
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/clone="cLECJolog"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XLI-Blue MRF'"
/clone_lib="tomato callus, TAMU"
/clone_lib="tomato callus, TAMU"
/note="Vector: pBlueScript SK(-); Site_l: EcoRl; Site_2:
Xhol; supplier: Giovannoni laboratory; cLEC - Cotyledons
of seedlings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Aixed callus was harvested at 25 and 40 days and included
Mixed callus was harvested callus EST Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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©
Generation of ESTs from tomato callus tissue Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Pred. No. 4.2e-65;
0; Mismatches 109;
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(mol_type="mRNA"
cultivar="TA496"
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                                                                                                                                                                                                                                                                                                          db_xref="taxon:4081"
clone="cLEC36D8"
tissue_type="callus"
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EST552012 tomato flower,
esculentum cDNA clone cTC
BI932123
BI932123.1 GI:16246595
EST.
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Best Local Similarity 75.7%;
Matches 339; Conservative
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and then
          Tracheophyta
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     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Track Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicot asterids; lamiids; Solanales; Solanaceae; Solanum; Lycoper 1 (bases 1 to 702)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Te Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Frase Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="flower"
/dev_stage="buds 8mm to preanthesis"
/clone_lib="tomato flower, 8 mm to preanthesis by
/clone_lib="tomato flower, 8 mm to preanthesis by
/note="Vector: pBluescript SK(-); Site_I: EcoRI;
XhoI; supplier: Cornell University; sequencing:
Institute for Genomic Research; Flower buds and
were taker from greenhouse plants (4-8 wks old,
They were immediately frozen in liquid nitrogen size-separated while remaining frozen."
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                                                                                                                                                                  Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
Institute
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 702
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                                                                                                                                                                                                                                                                                                                             organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109;
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                                                                                                                                                                                                                                                                                                                                          'mol_type="mRNA"
'cultivar="TA496"
'db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .702
                                                                                                                                                                                                                                                                                                                                                                                         clone="cTOC22G23"
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esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.1%;
larity 75.7%;
Conservative
                                                                                                                                                      (2001)
Lycopersicon
                                                                                                                                        preanthesis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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/dev stage="buds 8mm to preanthesis"
/clone lib="tomato flower, 8 mm to preanthesis buds"
/clone lib="tomato flower, 8 mm to preanthesis buds"
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants [4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                     Tracheophyta
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Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 736)
van der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J.,
Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M.,
Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, buds 8 mm -
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                               736 bp mRNA linear EST 18-OCT flower, 8 mm to preanthesis buds Lycopersicon clone cTOC24H17 5' end, mRNA sequence.
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University
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109;
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/clone="cTOC24H17"
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Best Local
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Xhol; supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 741)
van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E.,
Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Ronning, C.M.,
Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and
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AGTCATTGCCATGATAATTGAAGAGGCAAGAACTGGTGAAATAGGTGATGGAAAGATATT
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EST339498 tomato flower buds, anthesis, Cornell University Lycopersicon esculentum cDNA clone cTOD5K11 5', mRNA sequi
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Generation of ESTs from tomato flower tissue, anthesis
Unpublished (1999)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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/mol_type="mRNA"
/cultivar="TA496"
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larity 75.7%; Pred. No. 4.3e-65;
Conservative 0; Mismatches 109;
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/clone_lib="tomato flower buds,
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                                                                                                           GAGGATGACAGGAGGCGATCTGACATG 582
                                                                                                                                /db xref="taxon:4081"
/clone="cTOD5K11"
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